04/04/00 JC61 U.S. PTO

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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No.	EPI-067191
First Inventor or Application Identifier	Jonathan W. Nyce
Title	LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE...
Express Mail Label No.	EJ 664079305 US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: **Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231**

1. [✔] * Fee Transmittal Form *(e.g., PTO/SB/17)* *(Submit an original and a duplicate for fee processing)*
2. [✔] Specification [*Total Pages*] *(preferred arrangement set forth below)*
   - Descriptive title of the Invention
   - Cross References to Related Applications
   - Statement Regarding Fed sponsored R & D
   - Reference to Microfiche Appendix
   - Background of the Invention
   - Brief Summary of the Invention
   - Brief Description of the Drawings *(if filed)*
   - Detailed Description
   - Claim(s)
   - Abstract of the Disclosure
3. [ ] Drawing(s) *(35 U.S.C. 113)* [*Total Sheets*]
4. Oath or Declaration [*Total Pages*]
   a. [ ] Newly executed (original or copy)
   b. [ ] Copy from a prior application (37 C.F.R. § 1.63(d)) *(for continuation/divisional with Box 16 completed)*
      i. [ ] DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

NOTE FOR ITEMS 1 & 13: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

5. [ ] Microfiche Computer Program *(Appendix)*
6. Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all necessary)*
   a. [✔] Computer Readable Copy
   b. [✔] Paper Copy (identical to computer copy)
   c. [✔] Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

7. [✔] Assignment Papers (cover sheet & document(s))
8. [ ] 37 C.F.R.§3.73(b) Statement *(when there is an assignee)* [✔] Power of Attorney (2)
9. [ ] English Translation Document *(if applicable)*
10. [✔] Information Disclosure Statement (IDS)/PTO-1449 [✔] Copies of IDS Citations
11. [ ] Preliminary Amendment
12. [✔] Return Receipt Postcard (MPEP 503) *(Should be specifically itemized)*
13. [ ] * Small Entity Statement(s) *(PTO/SB/09-12)* [ ] Statement filed in prior application, Status still proper and desired
14. [ ] Certified Copy of Priority Document(s) *(if foreign priority is claimed)*
15. [✔] Other: checks, cover letter

16. If a CONTINUING APPLICATION, *check appropriate box, and supply the requisite information below and in a preliminary amendment.*

[X] Continuation [ ] Divisional [ ] Continuation-in-part (CIP) of prior application No: 60/127958

Prior application information: *Examiner* ______ *Group / Art Unit:* ______

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 4b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

17. CORRESPONDENCE ADDRESS

[ ] *Customer Number or Bar Code Label* *(Insert Customer No. or Attach bar code label here)* or [✔] *Correspondence address below*

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Signature	Viviana Amzel	*Date*	APRIL 4, 2000

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SEQ. BOX

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:		: Appl. Ref.:	EPI-067191
	Nyce et al	: Atty Ref.:	73999/01905
Appl. No:	not yet assigned	: Priority:	US 60/127,958
Filing Date:	herewith	:	

For: **LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONTRICTION, LUNCH INFLAMMATION, ALLERGY(IES) & SURFACTANT DEPLETION**

COVER LETTER

Box: New Application
Assistant Commissioner of Patents & Trademarks
Washington, DC 20231

Sir\Madam:

Enclosed for filing are the following:

1. Utility Patent Application Transmittal Form
2. Fee Transmittal Form
3. Assignments (2) and Recordation form and $40.00
4. U.S. Non-Provisional Paten Application
5. Sequence Listing, Declaration and diskette
6. IDS & 1449-PTO Form Listing References
7. Declarations (2)
8. Small Entity Status form
9. Postcard

Respectfully submitted.
ARTER & HADDEN

Viviana Amzel, Ph.D.
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213-617-9255 Fax

I hereby certify that this paper or fee is being deposited with the United States Postal Service **via Express Mail service in an Express Mail Package under label No. EJ664079305US** under 37 CFR 1.8 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington D C 20231, on April 4, 2000, by Jenny R. Wilson

Jenny R. Wilson

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS (37 CFR 1.9(f) AND 1.27 (d)) - NONPROFIT ORGANIZATION

Docket No. P66 42161

Serial No.	Filing Date	Patent No.	Issue Date
To Be Assigned	Herewith		

Applicant/ Patentee: Jonathan W. Nyce and W. James Metzger

Invention:

Low Adenosine Anti-Sense Oligonucleotide, Compositions, Kit & Method for Treatment of Airway Disorders Associated with Bronchoconstriction, Lung Inflammation, Allergy(ies) & Surfactant Depletion

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION: East Carolina University

ADDRESS OF ORGANIZATION: 103 Spilman Building
Greenville, North Carolina 27858

TYPE OF NONPROFIT ORGANIZATION:

- ☐ University or other Institute of Higher Education
- ☒ Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3))
- ☐ Nonprofit Scientific or Educational under Statute of State of The United States of America
  Name of State: Citation of Statute:
- ☐ Would Qualify as Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3)) if Located in The United States of America
- ☐ Would Qualify as Nonprofit Scientific or Educational under Statute of State of The United States of America if Located in The United States of America
  Name of State: Citation of Statute:

I hereby declare that the above-identified nonprofit organization qualifies as a nonprofit organization as defined in 37 C.F.R. 1.9(e) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in:

- ☐ the specification to be filed herewith.
- ☒ the application identified above.
- ☐ the patent identified above.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the above-identified nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed on the next page and no rights to the invention are held by any person, other than the inventor, who could not qualify as an independent inventor under 37 CFR 1.9(c) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

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☒ no such person, concern or organization exists.
☐ each such person, concern or organization is listed below.

FULL NAME ______________________________
ADDRESS ______________________________
☐ Individual ☐ Small Business Concern ☐ Nonprofit Organization

FULL NAME ______________________________
ADDRESS ______________________________
☐ Individual ☐ Small Business Concern ☐ Nonprofit Organization

FULL NAME ______________________________
ADDRESS ______________________________
☐ Individual ☐ Small Business Concern ☐ Nonprofit Organization

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Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: **Richard R. Eakin**

TITLE IN ORGANIZATION: **Chancellor**

ADDRESS OF PERSON SIGNING: **East Carolina University**
103 Spilman Building
Greenville, North Carolina 27858

SIGNATURE: Richard R. Eakin DATE: 4/21/99

LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION, ALLERGY(IES) & SURFACTANT DEPLETION

BACKGROUND OF THE INVENTION

Field of the Invention

This patent relates to a composition comprising oligonucleotides (oligos) that are anti-sense to adenosine receptors, and contain low amounts of or no adenosine (A). These agents are suitable for the treatment, among others, of pulmonary diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, allergic rhynitis, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

Background of the Invention

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the depletion reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A_1 receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A_1 receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor antagonist is available for clinical use attests to the general toxicity of these agents. Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding

an appropriate route of administration to deliver them to their site of action. Many in vivo experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature. Although anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as pharmacological agents in human disease, finding practical and effective applications for these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature. The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being an inherent difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%. Anti-sense oligonucleotides have been used in therapy by many, including the present inventor, who in his previous work successfully treated various diseases and conditions by direct administration of these agents to the lung. In many instances, other workers have had to face the difficulties associated with the delivery of DNA molecules to a desired target. Thus, the route of administration may be of extreme importance for treating generalized diseases and conditions as well as those which are localized. In contrast, up to the present time, the delivery of anti-sense agents to the lung has been relatively undeveloped. As described by the present inventor in more detail below, the lung is an excellent target for the direct administration of anti-sense oligonucleotides and provides a non-invasive and a tissue-specific route.

Clearly, there exist presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of adenosine mediated ailments afflicting the pulmonary and respiratory ailments affecting the lung airways, including respiratory problems, bronchoconstriction, inflammation, allergy(ies), depletion or hyposecretion of surfactant, etc., which is highly effective and sufficiently selective to avoid detrimental side effects produced by other therapies. In addition, there is a definite need for making available a delivery method that will require low amounts of therapeutic agents and will be effective for the rapid and targeted access of tissue genes of mRNAs and the reversal of untoward effects afflicting a subject.

SUMMARY OF THE INVENTION

The present invention generally relates to a pharmaceutical or veterinary composition, comprising an anti-sense oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies), and\or surfactant depletion and\or hyposecretion, when administered to a mammal, the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and a pharmaceutically or veterinarily acceptable carrier or diluent. The targets are typically molecules associated with airway disease, cancer, etc., such as transcription factors, stimulating and activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding proteins, and malignancy associated proteins, among others. Examples are oligo(s) targeted to adenosine receptor(s) and it(they) are typically

present in the composition in an amount effective to reduce adenosine mediated effect(s), such as airway obstruction, inflammation, allergy(ies), and sufactant depletion, among others. The adenosine receptor is preferably selected from the group consisting of the adenosine A_1, A_{2b}, and A_3 receptors, and in some instances even adenosine A_{2a} receptors. The oligo of the invention may be applied to the preparation of a medicament for (a) reducing adenosine-mediated bronchoconstriction, impeded respiration, inflammation, allergy(ies), depletion production of surfactant, and other detrimental pulmonary effects in a subject in need of treatment, and/or for (b) treating specific diseases and conditions such as asthma, cystic fibrosis, allergic rhynitis, COPD, etc. For the first time this invention provides the targeted administration of one or more oligonucleotides directly into the repiratory system. The oligos may be directed to any target and are intended for fast delivery through the mucosal tissue of the lungs for hybridization to a desired target polynucleotide, e. g. mRNA, to prevent gene transcription and translation, such that protein expression will be reduced, hampered, or completely stopped. Thus, this invention also provides a more general method for administering oligonucleotides that are anti-sense to targeted genes and mRNAs associated with any type of diseases, by direct administration into the respiratory system, e. g. by inhalation, by introduction of a solution or aerosol into the respiratory airways, and/or directly into the lung.

The present oligos, moreover, are suitable for reducing effects mediated by a variety of target proteins and genes, for example adenosine-mediated effects, including pulmonary, respiratory, and other associated effects, e. g. bronchoconstriction, inflammation, immune mediated reactions, allergy(ies) and other airway problems, which may be caused by different conditions, including cancer. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhynitis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), bronchitis, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agents are also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present agent is effectively administered prophylactically and therapeutically in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects. The oligo(s) may be administered by any means known to a subject, e. g. to the lungs of the subject, more generally through any and all systemic and topical routes. This oligonucleotide(s) (oligo(s)) employed are anti-sense to to a target DNA or RNA, e. g. an adenosine receptor DNA or RNA, and preferably consist essentially of up to about 15% adenosine (A), and more preferably contain no adenosine. The oligos are provided in the form of specific compositions and formulations, with a carrier or diluent, and optionally with other therapeutic agents and additives which are used for administration by specific routes, e.g. into the respiratory system, topically, transdermally, parenterally, by implantation, and the like. The oligo is also provided as a capsule or cartridge, and in the form of a kit. The oligos of the invention may be produced by selection of specific targeted segments of the gene or mRNA encoding the adenosine receptor as described below. In one preferred embodiment, the selection is made to obtain oligos that consisting essentially of less than about 15% adenosine (A). This may be done by selecting the target as done above, which includes genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxta-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, an alternative, e. g. a universal base(s) or other base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than about 15%, and down to no adenosine. Similarly, alternative and/or universal bases may be substituted for adenosine, e. g. specific

adenosine A1, A2b and A3 receptor antagonists or A2a receptor agonists, theophilline, enprophylline, and many other adenosine receptor antagonists known in the art as well as agonists with significantly reduced agonist activity with respect to adenosine, e. g. less than 0.5%, less than 0.3%, and the like.

The invent on will now be described in general in conceptual and experimental terms, with reference to specific examples. Other objects, advantages and features of the present invention will become apparent to those skilled in the art from the description that follows.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

This invention arose from a desire by the inventor to improve on prior art treatments for pulmonary and other diseases, which technology is generally frought with detrimental side effects and by the need of administering high doses of therapeutical agents. The present invention arises from the inventor's own discovery that adenosine receptor targeted anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation and/or allergy(ies), constrict bronchial tissue, obstruct the lung airways, depletion surfactant secretion, or otherwise impede normal breathing. In general, many diseases and conditions are associated with or cause inflammation, constrict bronchial tissue or the lung airways, depletion secretion of surfactant, augment allergy(ies), or otherwise impede normal breathing. This treatment is selective for specific targets associated with or mediating these symptoms, and the agents are administered in up to 1000-fold lower doses than those seen in the art. The inventor, in addition, wanted to provide a treatment which would improve the outcome and life style of patients undergoing other procedures or being administered other therapies, including antibody therapy, chemotherapy, radiation, phototherapy, and surgery e.g. cancer surgery, and that could be effectively administered preventatively, prophylactically or therapeutically. He reasoned that he could further improve on this discovery by selecting oligos of reduced adenosine content, or reducing the adenosine content of otherwise targeted anti-sense oligos corresponding to endogenous polynucleotide sequences. The present invention is premised on the discovery by the inventor that oligonucleotides are metabolized in vivo to their mononucleotides. Adenosine (A)-containing oligonucleotides break down and release adenosine which, in turn, activates adenosine receptors, thereby causing bronchoconstriction, inflammation, surfactant depletion, allergy(ies), and the like. He, thus, conceived of employing low adenosine-free adenosine oligos to avoid these side effects upon their administration. He succeeded in this endeavor and is providing in this patent novel and improved compositions, formulations and methods which afford greatly improved results when compared with previously known treatments for preventing and alleviating bronchoconstriction, allergy(ies), inflammation, breathing difficulties, surfactant depletion and blockage of airways, as well as for other conditions which affect the lung directly or indirectly. In different embodiments, one or more nucleic acids of the invention may be formulated alone, and/or with one or more surfactant components and/or with a carrier, and/or with other therapeutic agents and/or formulation agents known in the art. The compositions of this invention, thus, may be incorporated into a variety of formulations for systemic and topical administration. Moreover, the inventor also provides a broad method for delivery of anti-sense oligonucleotides (ol gos) through the respiratory system, as a fast means of starting treatment to address acute attacks of asthma and other diseases and conditions that have a rapid onset. In addition, the present agents have long ha flives and may be administered at very low doses. This makes them ideal for once a week type therapies. In the past, anti-sense oligonucleotides received considerable theoretical consideration as being potentially useful as pharmacologic agents for the treatment of human disease. Wagner, R., Nature 372: 333-335 (1994). However, it has been difficult to actually apply these molecules to alleviating and curing human diseases. One important consideration in the pharmacologic application of these molecules has been the failure of various routes of administration to deliver the compounds to its target while avoiding invading the circulation and, therefore, other untargeted tissues which, thus, produces a plethora of side effects. Most in vivo experiments utilizing anti-sense oligonucleotides involved a direct application of the ol go to limited regions of the brain. See, Wahlestedt, C., Trends in Pharmacol. Sci. 15: 42-46 (1994); Lai, .. et al., Neuroreport 5: 1049-1052 (1994); Standifer, K., et al., Neuron 12: 805-810

(1994); Akabayashi, A., et al., Brain Res. 21: 55-61 (1994). Others applied them into the spinal fluid. See, e.g. Tseng, L., et al., European J. Pharmacol. 258: R1-3 (1994); Raffa, R., et al., European J. Pharmacol. 258: R5-7 (1994); Gillardon, F., et al., European J. Neurosci. 6: 880-884 (1994). Such applications, clearly, have no practical clinical utility due to their invasive nature. Thus, the systemic administration of anti-sense oligonucleotides poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues. The systemic administration of anti-sense oligonucleotides also poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues.

The respiratory system, and in particular the lung, as the ultimate port of entry into the organism, however, is an excellent route of administration for anti-sense oligonucleotides. This is so not only for the treatment of lung disease, but also when utilizing the lung as a means for delivery, particularly because of its non-invasive and tissue-specific nature. Thus, local delivery of antisense oligonucleotides directly to the target tissue enables the therapeutic use of these compounds. Fomivirsen (ISIS 2302) is an example of a local drug delivery into the eye to treat cytomegalovirus (CMV) retinitis, for which a new drug application has been filed by ISIS. The administration of a drug through the lung offers the further advantage that inhalation is non-invasive whereas direct injection in to the vitreous of the eye is invasive. The composition and formulations of this invention are highly efficacious for preventing and treating diseases and conditions associated with bronchoconstriction, difficult breathing, impeded and obstructed lung airways, allergy(ies), inflammation and surfactant depletion, among others. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The invention will be described with respect to the adenosine receptors as targets, but is similarly applicable to any other target with respect to the pulmonary administration of anti-sense oligos. The examples provided below show a complete inhibition of such adenosine receptor associated symptoms in a rabbit model for human bronchoconstriction, allergy(ies) and inflammation as well as the elimination of the ability of the adenosine receptor agonist par excellence, adenosine, to cause bronchoconstriction in hyper-responsive monkeys, which are animal models for human hyper-responsiveness to adenosine receptor agonists. The pharmaceutical composition and formulations of the invention, therefore, are suitable for preventing and alleviating the symptoms associated with stimulation of adenosine receptors, such as the adenosine A_1 receptors. The compositions and formulations of this invention, thus, are also suitable for preven the untoward side effects of adenosine-mediated hyperresponsiveness in certain individuals, which are generally seen in diseases affecting respiratory activity.

The method of the present invention may be used to treat airway diseases and conditions in a subject of any kind and for any reason, with the intention that the adenosine content of anti-sense compounds be minimized, reduced or eliminated so as to prevent its liberation upon anti-sense degradation. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the compositions and formulations of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, allergic rhynitis, impeded respiration, Acute Respiratory Distress Syndrome (ARDS), renal damage and failure associated with ischemia as well as the administration of certain drugs, side effects associated with adenosine administration e.g. in SupraVentricular Tachycardia (SVT) and in adenosine stress tests, infantile Respiratory Distress Syndrome (infantile RDS), ARDS, pain,

cystic fibrosis, pulrionary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rjejection, pulmonary infections, and cancers such as leukemias, lymphorr as, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, metastatic cancer such as hepatic metastases, lung, breast and prostate metastases, among others. The present compositions and formulations are suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present compositions and formulations may also be administered effectively as a substitute for therapies that have significant negative side effects.The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. For consistency=s sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids). Nucleotide sequences are presented herein by single strand only, in the 5' to 3' direction, from left to right. In addition, nucleotide and amino acids are represented herein in the manner recommended by the IUPAC-IUB Biochemical Nomenclature Commission, or (for amino acids) by three letter code, in accordance with 37 CFR ' 1.822 and established usage. See, e.g., PatentIn User Manual, 99-102 (Nov. 1990) (U.S. Patent and Trademark Office, Office of the Assistant Commissioner for Patents, Washington, D.C. 20231); U.S. Patent No. 4,871,670 to Hudson et al. at col. 3, lines 20-43. The present method utilizes anti-sense agents to inhibit or down-regulate gene expression of target genes, including those listed in Tables 1 and 2 below. This is generally attained by hybridization of the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide or asnti-sense oligo" is generally a short sequence of synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein. The terms "desAdenosine" (desA) and "des-thymidine" (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des A or des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another lacking its undesirable activity, such as acting as an agonist or having a triggering effect at the adenosine A receptor(s). In the present context, the substitution is generally accomplished by substitution of A with a "universal or alternative base", presently known in the art or to be ascertained at a later time. As used herein, the terms "prevent", "preventing", "treat" or "treating" refer to a preventative, prophylactic, maintenance, or therapeutic treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms associated with adenosine receptor stimulation. The term "down-regulate" refers to inducing a decrease in production, secretion or availability and, thus, a decrease in concentration, of intracellular target product, be it a receptor e. g. adenosine A_1, A_{2b}, A_3, bradykinin 2B, GATA-3, or other receptors, or an increase in concentration of the adenosine A_{2a} receptor. The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to

design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with an alternative or a universal base, or an adenosine analog incapable of significantly, or having substantially reduced ability for, activating or antagonizing adenosine $A_{1,}$ A_{2b} or A_3 receptors or which may act as an agonist at the adenosine A_{2a}, receptor. Any number of adenosines present may be substituted by an alternative and/or universal base, such as heteroaromatic bases, which binds to a thymidine base but has less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A_1, A_{2a}, A_{2b} and A_3 receptors. Based on his prior experience in the field, the inventor reasoned that in addition to "downregulating" specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of a mRNA molecule which encodes a protein associated with impeded breathing, allergy(ies), lung inflammation, depletion of lung surfactant or lowering of lung surfactant, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject=s lung. In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, α= methoxy ethyl and similar modifications, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See, Milligan et al.; Cohen, J. S. D., supra. In another preferred embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See Tidd, D. M. and Warenius, H.M., Be. J. Cancer 60: 343-350 (1989); Shaw, J.P. et al., Nucleic Acids Res. 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention, as do α' modifications, such as α' methoxy ethyl, and the like. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See, Milligan, et al., supra. In addition, a plurality of substitutions to the carbohydrate ring are also known to improve stability of nucleic acids. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, supra. Preferred backbone analogue residues include phosphoramidate, phosphorothioate, methylphosphonate, phosphorotriester, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal, triformacetal, thioether, carbamate, boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, C_5-substituted nucleotides, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), methoxymethyl (MOM), and methoxyethyl(MOE), and methyleneoxy(methylimino) (MOMI) residues, and combinations thereof. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, supra. Where appropriate, the agent of this

invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable salts is administered. A single agent of this invention has the capacity to attenuate the expression of a target mRNA and/or various agents to enhance or attenuate the activity of a pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mononucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, i.e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i.e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As. The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region. The flanking regions of the exons may also be targeted as well as the spliced segments in the precursor mRNAs. The mRNA sequences of the adenosine receptors and of many other targets are derived from the DNA base sequence of the gene expressing either receptors, e. g. the adenosine receptors, the enzymes, factors, or other targets associated with airway disease. For example, the sequence of the genomic human A_1 adenosine receptor is known and is disclosed in U.S. Patent No. 5,320,963 to Stiles, G., et al. The A_3 adenosine receptor has been cloned, sequenced and expressed in rat (see, Zhou, F., et al., P.N.A.S. (USA) 89: 7432 (1992)) and human (see, Jacobson, M. A., et al., U.K. Patent Application No. 9304582.1 (1993)). The sequence of the adenosine A_{2b} receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., Genomics (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the remaining exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques. The sequences for the adenosine A_{2a} bradykinin, and other genes as well as methods for preparation of oligonucleotides are also known as those of many other target genes and mRNAs for which this invention is suitable. Thus, anti-sense oligonucleotides that downregulate the production of target sequences associated with airway disease, including the adenosine A_1, A_{2a}, A_{2b}, A_3, bradykinin, GATA-3, COX-2, and many other receptors, may be produced in accordance with standard techniques. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress

syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer.

The adenosine receptors discussed above are mere examples of the high power of the inventor=s technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is one associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 and Table 2 below, among others. The anti-sense agent(s) of the invention have a low A content to prevent its liberation upon in vivo degradation of the agent(s). For example, if the system is the pulmonary or respiratory system, a large number of genes is involved in different functions, including those listed in Table 1 below.

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1β (IL-1β)
Interleukin-1β Receptor (IL-1βR)	Eotaxin
Tryptase	Major Basic Protein
β2-adrenergic Receptor Kinase	Endothelin Receptor A
Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesion Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule
Substance P	(VCAM)
Rantes	Endothelial Leukocyte Adhesion Molecule Endothelin ETA
Receptor	(ELAM-1)
Cyclooxygenase-2 (COX-2)	GM-CSF, Endothelin-1
Monocyte Activating Factor	Neutrophil Chemotactic Factor
Neutrophil Elastase	Defensin 1,2,3
Muscarinic Acetylcholine Receptors	Platelet Activating Factor
Tumor Necrosis Factor α	5-lipoxygenase
Phosphodiesterase IV	Substance P
Substance P Receptor	Histamine Receptor
Chymase	CCR-1 CC Chemokine Receptor
Interleukin-2 (IL-2)	Interleukin-4 (IL-4)
Interleukin-12 (IL-12)	Interleukin-5 (IL-5)
Interleukin-6 (IL-6)	Interleukin-7 (IL-7)
Interleukin-8 (IL-8)	Interleukin-12 Receptor (IL-12R)
Interleukin-7 Receptor (IL-7R)	Interleukin-1 (IL-1)
Interleukin-14 Receptor (IL-14R)	Interleukin-14
CCR-2 CC Chemokine Receptor	CCR-3 CC Chemokine Receptor
CCR-4 CC Chemokine Receptor	CCR-5 CC Chemokine Receptor
Prostanoid Receptors	GATA-3 Transcription Factor
Neutrophil Adherence Receptor	MAP Kinase
Interleukin-15 (IL-15)	Interleukin-15 Receptor (IL-15R)

Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
NFAT Transcription Factors	STAT 4
MIP-1α	MCP-2
MCP-3	MCP-4
Cyclophillin (A, B, etc.)	Phospholipase A2
Basic Fibroblast Growth Factor	Metalloproteinase
CSBP/p38 MAP Kinase	Tryptase Receptor
PDG2	Interleukin-3 (IL-3)
Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
FK506-Binding Protein	α4β1 Selectin
Fibronectin	α4β7 Selectin

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

cMad CAM-1	LFA-1 (CD11a/CD18)
PECAM-1	LFA-1 Selectin
C3bi	PSGL-1
E-Selectin	P-Selectin
CD-34	L-Selectin
p150,95	Mac-1 (CD11b/CD18)
Fucosyl transferase	VLA-4
STAT-1	STAT-2
CD-18/CD11a	CD11b/CD18
ICAM2 and ICAM3	C5a
CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
LTB-4	AP-1 Transcription Factor
Protein kinase C	Cysteinyl Leukotriene Receptor
Tachykinnen Receptors (tach R)	I6B Kinase 1 & 2
Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
STAT 6	c-mas
NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
Medullasin	Interleukin-16 Receptor (IL-16R)
Adenosine A_1 Receptor (A_1 R)	Tryptase-I
Adenosine A_{2b} Receptor (A_{2b} R)	Adenosine A_3 Receptor (A_3 R)
β Tryptase	STAT-3
Adenosine A_{2a} Receptor (A_{2a} R)	IgE Receptor β Subunit (IgE R β)
Fc-epsilon receptor CD23 antigen	IgE Receptor α Subunit (IgE R α)
IgE Receptor Fc Epsilon Receptor (IgERFc ξ R)	Substance P Receptor
Histidine decarboxylase	Tryptase-1
Prostaglandin D Synthase	Eosinophil Cationic Protein
Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
Neutrophil Oxidase Factor	Cathepsin G
Macrophage Inflammatory Protein-1-	Interleukin-8 Receptor α Subunit (IL-8 Rα)
Alpha/Rantes Receptor	Endothelin Receptor ET-B

These genes, and others, are involved in the normal functioning of respiration as well as in diseases associated with respiratory pathologies, including cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, chronic bronchitis, respiratory distress syndrome (ARDS), allergic rhinitis, lung cancer and lung metastatic cancers and other airway diseases, including those with inflammatory response.

Anti-sense oligos to the target receptors, e. g. the adenosine A_1, A_{2a}, A_{2b}, and A_3 receptors, CCR3 (chemokine receptors), bradykinin 2B, CAM (vascular cell adhesion molecule), and eosinophil receptors,

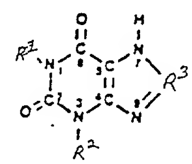
among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A_1, A_{2a}, A_{2b}, and/or A_3 receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents may be utilized by the present method alone or in conjunction with anti-sense oligos targeted to other genes to validate pathway and/or networks in which they are involved. For better results, the oligos are preferably administered directly into the respiratory system, e.g., by inhalation or other means, of the experimental animal, so that they may reach the lungs without widespread systemic dissemination. This permits the use of low agent doses as compared with those administered systemically or by other generalized routes and, consequently, reduces the number and degree of undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. Anti-sense oligonucleotides to the A_1 , A_{2b}, A_3, bradykinin B2, GATA-3, CAM (vascular cell adhesion molecule), eosinophil receptors, and COX-2 receptors, among others, have been shown to be effective in the down-regulation of the respective receptor proteins in the cell. One novel feature of this treatment, as compared to traditional treatments for adenosine-mediated bronchoconstriction, is that administration is direct to the lungs, or in situ to other tissues, organs or systems of the body. Additionally, a receptor protein itself is reduced in amount, rather than merely interacting with a drug, and toxicity is reduced. Other proteins that may be targeted with anti-sense agents for the treatment of lung conditions include, but are not limited to: CCR3 (chemokine) receptors, human A_{2a} adenosine receptor, human A_{2b} adenosine receptor, human IgE receptor β, human Fc-epsilon receptor CD23 antigen, human histidine decarboxylase, human beta tryptase, human tryptase-I, human prostaglandin D synthase, human cyclooxigenase-2, human eosinophil cationic protein, human eosinophil derived neurotoxin, human eosinophil peroxidase, human intercellular adhesion molecule-1 (ICAM-1), human vascular cell adhesion molecule-1 (VCAM-1), human endothelial leukocyte adhesion molecule-1 (ELAM 1), human P selectin, human endothelial monocyte activating factor, human IL-3, human IL-4, human IL-5, human IL-6, human IL-8, human monocyte-derived neutrophil chemotactic factor, human neutrophil elastase, human neutrophil oxidase factor, human cathepsin G, human defensin 1, human defensin 3, human macrophage inflammatory protein-1-alpha, human muscarinic acetylcholine receptor HM3, human fibronectin, human GM-CSF, human tumor necrosis factor α, human leukotriene C4 synthase, human major basic protein, and human endothelin 1. Although not intended to be exclusive, a more extensive list of genes is provided below. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A_1, A_{2a}, A_{2b}, and/or A_3 receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. In these latter targets, and in target genes in general, it is particularly imperative to eliminate or reduce the adenosine content of the corresponding anti-sense oligonucleotide to prevent their breakdown products from liberating adenosine.

As used herein, the term "treat" or "treating" asthma refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of the lung disease. The term "downregulate" refers to inducing a decrease in production, secretion or availability (and thus a

decrease in concentration) of the targeted intracellular protein. The present invention is concerned primarily with the treatment of human subjects. However, the agents and methods disclosed here may also be employed for veterinary purposes, such as is the case in the treatment of other mammals, such as cattle, horses, wild animals, zoo animals, and domestic animals, e. g. dogs and cats. Targeted proteins are preferably mammalian and more preferably of the same species as the subject being treated. In general, "anti-sense" refers to the use of small, synthetic oligonucleotides, resembling single-stranded DNA, to inhibit gene expression by inhibiting the function of the target messenger RNA (mRNA). Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993). In the present invention, inhibition of gene expression of the A_1 or A_3 adenosine receptor is desired. Gene expression is inhibited through hybridization to coding (sense) sequences in a specific messenger RNA (mRNA) target by hydrogen bonding according to Watson-Crick base pairing rules. The mechanism of anti-sense inhibition is that the exogenously applied oligonucleotides decrease the mRNA and protein levels of the target gene or cause changes in the growth characteristics or shapes of the cells. Id. See, also Helene, C. and Toulme, J., Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC Press: Boca Raton, FL (1987). As used herein, "anti-sense oligonucleotide" is defined as a short sequence of synthetic nucleotide that (1) hybridizes to any coding sequence in an mRNA which codes for the targeted protein, according to hybridization conditions described below, and (2) upon hybridization causes a decrease in gene expression of the A_1 or A_3 adenosine receptor. The receptors discussed above are mere examples of the high power of the present technology. In fact, a large number of genes may be targeted in a similar manner by practicing the present methods, to significantly down-regulate or obliterate protein expression and observe any changes wrought to one or more functions within a system, e.g. the respiratory system and other lung disease associated targets. By means of example, in the respiratory system, the targets may be associated with difficulties of breathing, bronchoconstriction, inflammation, allergic rhynitis, chronic bronchitis, surfactant depletion, and others associated with diseases and conditions such as chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, inhalation burns, Acute Respiratory Distress Syndrome (ARDS), cystic fibrosis, pulmonary fibrosis, radiation pulmonitis, tonsilitis, emphysema, dental pain, oral inflammation, joint pain, esophagitis, cancers afflicting the respiratory system either directly such as lung cancer, esophageal cancer, and the like, or indirectly by means of metastases, among others. These functions are of great interest because of their association with respiratory dysfunction, as is the case in asthma, allergies, allergic rhinitis, pulmonary bronchoconstriction and hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis (CF), Acute Respiratory Distress Syndrome (ARDS) as well as infantile and pregnancy-related RDS, cancer, etc., which either directly or by metastasis afflict the lung, the present anti-sense oligonucleotides may be directed to a list of target mRNAs, which includes the targets listed in Table 1 above, among others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C and/or having a specific type and/or extent of activity, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a thymidine (T) nucleic acid content of up to and including about 15%, preferably, about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no thymidine. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%, preferably about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no adenosine. When the selected fragment comprises at least one thymidine base, an adenosine base may be substituted in the corresponding anti-sense nucleotide fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about bout 10%, preferably less than about 1%, and more preferably less than about 0.3% of the adenosine base agonist activity at the adenosine A_1, A_{2a}, A_{2b} and A_3 receptors, and heteroaromatic bases which have no activity at the adenosine

A_{2a} receptor, when validating in the respiratory system. Other adenosine activities in other systems may be determined in other systems, as appropriate. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH_2, SH, SO, SO_2, SO_3, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkyny aryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH_2, primary, secondary and tertiary amine, SH, SO, SO_2, SO_3, cycloalkyl, heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R^1 and R^2 are independently H, alkyl, alkenyl or alkynyl and R^3 is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH_2-alkylamino-ketoxyalkyloxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO_2aryl, among others. Similar modifications in the sugar are also embodiments of this invention. Reduced adenosine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA serves to prevent the breakdown of the oligos into products that free adenosine into the system, e.g. the lung, brain, heart, kidney, etc., tissue environment and, thereby, to prevent any unwanted effects due to it. By means of example, the Nf6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or desthymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above, in Table 2 below, and others associated with functions of the brain, cardiovascular and renal systems, and many others. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B transcription factor, typically about 10 to 30 sequences may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenosine content may suffice to render the anti-sense oligonucleotide less active or even inactive against the target. In accordance with this invention, these so called "non-fully desA" sequences may preferably have a content of adenosine of less than about 15%, about 12%, about 10%, about 7%, about 5%, and about 2% adenosine. Most preferred is no adenosine content (0%). In some instances, however, a higher content of adenosine is acceptable and the oligonucleotides still fail to show detrimental "adenosine activity". A particular important embodiment is that where the adenosine nucleotide is "fixed" or replaced by a "Universal or alternative" base that may base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T.

A universal or alternative base is defined in this patent as any compound, more commonly an

adenosine analogue. which has substantial capacity to hybridize to thymidine, while at the same time having reduced, or substantially lacking, ability to bind adenosine receptors or other molecules through which adenosine may exert an undesirable side effect in the experimental animal or in a cell system. Alternatively, adenosine analogs which completely fail to activate, or have significantly reduce ability for activating, adenosine receptors, such as the adenosine A_1, A_{2b} and/or A_3 receptors, most preferably A_1 receptors, and those that may even act as agonists of the adenosine A_{2a}, receptor, may be used. One example of a universal base is α-deoxyribofuranosol-(5-nitroindole), and an artisan will know how to select others. This "fixing" step generates further novel sequences, different from those anti-sense to the ones found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. Other examples of universal or alternative bases are 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3 - nitropyrrole - 2' - deoxynucleoside, 5 - nitro-indole, 2 - deoxyribosyl - (5 - nitroindole), 2-deoxyribofuranosyl - (5-nitroindole), 2' - deoxyinosine, 2' -deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4, 5 - c] oxazine - 7 - one and 2 - amino - 6 -methoxy aminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3 - nitropyrrole 2' - deoxynucleoside 2 - deoxyribofuranosyl - (5 - nitroindole), 2' - deoxyinosine and 2' - deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H - 3, 4 - dihydropyrimido [4,5 - c] [1, 2] oxazin - 7 - one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2 - amino - 6 - methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art or will become available are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl. Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem.260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992; Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon , M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (10): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding being incorporated herein by reference. When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% "desA" anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be "fixed" by replacement with a "Universal" or "replacement" base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A. Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

Table 2: Cancer Targets

Transforming Oncogenes	**Therapy Targets**
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl 2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase
Angiogenesis factors	Adhesion Molecules
Oncogenes	Folate Pathway Enzymes
DNA repair genes	(One Carbon Pool)
	Telomerase
	HMG CoA Reductase
	Farnesyl Transferase
	Glucose-6-Phosphate Transferase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or hose generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like. The present technology is particularly useful in the treatment of cancer ailments given that traditiona cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desirec pathway or target. This approach provides a significant advantage over standard treatments of cance because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells that, for instance, express all three targets while normal cells that may expresses only one or two of the targets will be significantly less affected or even spared. A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensines, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions. Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1α, MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophillins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1,CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well. In another embodiment, at least one of the mRNAs to which the oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors, adenohypophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated. The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A_1 receptor, adenosine A_2B receptor, adenosine A_3 receptor, endothelin receptor A, endothelin receptor B, IgE high affinity receptor, muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1β receptor (IL-1βR), interleukin-1 receptor (IL-1R), interleukin-1β receptor (IL-

1βR), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, parasympathomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein. The encoded enzymes for development of the oligos of the invention include synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and , polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase, β2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipooxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil elastase, phospholipase A_2, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition, however, is suitable as a target for this invention. Suitable encoded factors for application of this invention are, among others, Nf6B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor α (TNF α), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned. Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein. Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1β (IL-1β), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11),CCR-5 CC chemokine, and Rantes. Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation. Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are α4β1 selectin, α4β7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcBCL. Others, however, are also suitable for use with this invention.

The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence=s total number of nucleotides. These fragments

may be selected from any portion of the longer oligo, for example, from the middle, 5'- end, 3'- end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenosines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal or alternative base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A_1 and/or A_3 receptors. In fact, such replacement nucleotide acts as a "spacer". Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60.

<u>Human Receptor-related Antisense Polynucleotide</u>

5'-GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C TGCTTTTCT TTTCTGGGCC
TCTGTGGTCT GTTTTTTTCT GGCCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCCBTGB
TGGGCBTGCC GTCGTTCTTG CCCTCCTTTG GCTGCCGTGC CCGCTCCCCG GCCTCCTGGC GGGTGGCCGT
TGGGCCCGTG TTCCCCTGGG GCCTGGGGCT CCCTTCTCTC GCCCTTCTTG CTGGGCCTCT GCTGCTGCTG
GTGCTGTGGC CCCCCGTACA CCGAGGAGCC CATGATGGGC ATGCCACAGA CGACAGGCGT BCBCCGBGGB
GCCCBTGBTG GGCBTGCCBC BGBCGBCBGG C GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC
CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC
CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG
CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG
CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC ACA
GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT
CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT
TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC
CC TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT GCC
TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT
GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG
TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG
AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB
TGG CGG TCC TGC TTG GBT TCT CCC GB GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA
GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC
TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT
TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT
TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT
TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GCC TGT
GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG
G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG
BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA
TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB
TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC
TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC

CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG
GGC TGC GTG CGC GTT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC
GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG
CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC
CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA
GAC AGG GCA GGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC
GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC
BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT
CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG
GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC
TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG
CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG
GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT
TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA
GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC
GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G CTCAGTGGCC
CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTTACT ATGAGGCCGT GTCTGTCGTG
TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCGT GTCTTTCCTT
TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTTCC TTTGCTCTTG
GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC
TCGGCCCCGC GCCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC
GGCGCTGCCC TGCCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC
GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG
GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC
GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC
GGTTGTGGCT CGGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT
GCCCCTCTCC TCTCCTTCCT CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG
GCTTTTTTTC TCTTCCTCCT TTTTCGTGCG TGGGCCTCC GCACGCCTCT TGCCACCTCC TGCGCAGGGC
AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG
CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCCTC
CTGCGCBGGG CBGCGCCTTG GGGCCBGCGC CGCTCCCGGC GCGGCCBGCB GGGCBGCCBG CBGCGCGCBG
CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C GCTGCCCGGC
GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC
TTCGTCCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCCT CGGGGTCCCG
GGGCTTCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGTG GCTBGGTGGG GC GGG GTG GGT
BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT
TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT
TGGCG CTG GCG GGG GGG CCT CCTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG
TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG
CCGGG GTG GGT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT GCA GGG G
ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG
GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB
CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTC BTCBBBBTCC CBCBTCTGTG
GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG
TGGCTCGGTG CTTCTGCCCC TGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC
CTCTTTCTCT TTGTTCGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTCC GCCCTGTCGG GCGGGAAGCC
TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG
ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGCGCC CTGTCGGGCG
GGBBGCCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC BGCGCBBCCB GGGCGCGTCC
GCBCBGBCTT GGBGGCGGCT GCBTGCTGCT BCCTGCTCGGGCG GGBBGCCTCCG GTGGCCGCCG CGCGTCCGGT
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Human Enzyme-related Antisense Polynucleotide

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Human Factor Related Anti-sense Oligonucleotide

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(SEQ. ID NO:3004)

<u>Human Adenosine A_1 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments</u>

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GAGGACTCTG GACCCCAGGC CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA

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CBC GC GGC CTG G GGB GGG CGG C GBT GGB GGG GG CTG GGC GC GGC CTG GAA AGC TGA GAT GGA GGG
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GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3'**(FRAG.NO:__)(SEQ.NO:3005) [2423)]**

5'-CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGGT TTGGGTTGTT GTTGTTGTTG TTTGGTGTGT TTTTTGTTTT TTTGTTTTTT TGTTTTTTTT TGAGATGGAG TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC AGCCAGCTAC CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG AGCTAGCGGC TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC CGGGAGCTCT GCCAGCTTTG GTGACCTTGG GTGCTTGCCT CGTGCCCCTT GGTGCCCGTC TGCTGATGTG CCCAGCCTGT GCCCGCCATG CCGCCCTCCA TCTCAGCTTT CCAGGCCGCC TACATCGGCA TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC TGGGCGGTGA AGGTGAACCA GGCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTCGCTG GCGGTGGCTG ATGTGGCCGT GGGTGCCCTG GTCATCCCCC TCGCCATCCT CATCAACATT GGGCCACAGA CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCCT CATCCTCACC CAGAGCTCCA TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC CCTCTCCGGT ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC TGGATCCTCT CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG GTGGAGCGGG CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC GAGAAGGTCA TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC ATCCTCAACT GCATCACCCT CTTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC ATCCAGAAGT TCCGCGTCAC CTTCCTTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC GCTCCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGCGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCCTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3' **(FRAG. NO:__)(SEQ. ID NO: 2434)**

5'- ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGCAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTTC CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCCACA TCCAGTGGGG TCTCAGTCCA GTCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG GGCTGTTGGC TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG GACCAGGTGT CTAGAGGCAA CAGTGTTCTG AGCCCCCACC TGCCTGACCA TCCCATGAGC AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCCAGGC CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC

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5'- ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
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(FRAG. NO:__)(SEQ. ID NO: 2432)

5'-CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA AGGAAAATTT
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CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG GTGGAGCGGG CCTGGGCAGC
CAACGGCAGC ATGCGGGAGC CCGTGATCAA GTGCGAGTTC GAGAAGGTCA TCAGCATGGA GTACATGGTC
TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC TCATGGTCCT CATCTACCTG GAGGTCTTCT
ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA
GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC
ATCCTCAACT GCATCACCCT CTTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT
TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC ATCCAGAAGT TCCGCGTCAC
CTTCCTTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCCAGAA
GAGAGGCCTG ATGACTAGAC CCCGCCTTCC GCTCCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC
TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG
AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC
TGCAGGAGGC CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC
CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCCTGGGG AGGCTGAGAC
TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTC
TTAGATGTTG GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA
AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3'
(FRAG. NO:__)(SEQ. ID NO: 2422)

5'-ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA
GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG
GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG
AGCGCTGCGG CGGCAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG
CGCGGCCCGG AGCTCTGTTC CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG
ATGGTGCTTG CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT

CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA
CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCG
CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC
AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC
CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT
TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT
CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG
CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA
AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC
CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC
CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA
ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT
CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT
TCCGCTCCCA CCAGCCCACA TCCAGTGGGG TCTCAGTCCA GTCCTCACAT GCCCGCTGTC CCAGGGGTCT
CCCTGAGCCT GCCCCAGCTG GGCTGTTGGC TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT
GTGGTCCCTC CACTAGGAGT TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT
CCTACGGAGG GACCAGGTGT CTAGAGGCAA CAGTGTTCTG AGCCCCCACC TGCCTGACCA TCCCATGAGC
AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG
AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG
ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG ATGCACTGGC
CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT
GAGGACTCTG GACCCCAGGC CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA
TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC
ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC
CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACCAGCTC
CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG GCCTGATGGA
GAGGAGAACA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT
CTGTAAGGAC TCACTGTTGA CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG
AGTACCCCCC TGACAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG
GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA
TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC
TGGAGCCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA GGCGGGGGAT
CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC
AACTCCAGGA CTTCCTTCCA AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
CCATGTGACT AATAAAAAAC TGTGAACCCT -3' **(FRAG. NO:__) (SEQ. ID NO: 2421)**

5'-ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
TGCCCGGGAA CGTCCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT
CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC
ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT
CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT
GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG
AGCCCGTGAT CAACTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT
GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG
CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA
AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC
CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC
TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA
ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G

(FRAG NO: __) (SEQ. ID NO: 2420)

5'-GAT GGA GGG CGG CAT GGC GGG-3' **(FRAG. NO: 1657) (SEQ ID NO:2412)**
5'-G CGG GTC GCC GC-3' **(FRAG. NO: 1658) (SEQ ID NO:2413)**
5'-GGC GGG CBC BGG C-3' **(FRAG. NO: 1659) (SEQ ID NO:2414)**
5'-GGC GGG CBC-3' **(FRAG. NO: 1660) (SEQ ID NO:2415)**
5'-GC GGC CTG G-3' **(FRAG. NO: 1661) (SEQ ID NO:2416)**
5'-GGB GGG CGG C-3' **(FRAG. NO: 1662) (SEQ ID NO:2417)**
5'-GBT GGB GGG-3' **(FRAG. NO: 1663) (SEQ ID NO:2418)**
5'-GG CTG GGC-3' **(FRAG. NO: 1664) (SEQ ID NO:2419)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' **(FRAG.1) (SEQ. ID NO: 11)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' **(FRAG 2) (SEQ. .ID NO:12)**

5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3'(FRAG 3)(SEQ.ID NO:13)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 4)(SEQ. ID NO:14)
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 5) (SEQ. ID NO: 15)
5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 6) (SEQ. ID NO: 16)
5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 7) (SEQ. ID NO: 17)
5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 8) (SEQ. ID NO: 18)
5'-GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 9) (SEQ. ID NO: 19)
5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 10) (SEQ. ID NO: 20)
5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 11) (SEQ. ID NO: 21)
5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 12) (SEQ. ID NO: 22)
5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 13) (SEQ. ID NO: 23)
5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 14) (SEQ. ID NO: 24)
5'-TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 15) (SEQ. ID NO: 25)
5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 16) (SEQ. ID NO: 26)
5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 17) (SEQ. ID NO: 27)
5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 18) (SEQ. ID NO: 28)
5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 19) (SEQ. ID NO: 29)
5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 20) (SEQ. ID NO: 30)
5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 21) (SEQ. ID NO: 31)
5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 22) (SEQ. ID NO: 32)
5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 23) (SEQ. ID NO: 33)
5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 24) (SEQ. ID NO: 34)
5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 25) (SEQ. ID NO: 35)
5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 26) (SEQ. ID NO: 36)
5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 27) (SEQ. ID NO: 37)
5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 28) (SEQ. ID NO: 38)
5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 29) (SEQ. ID NO: 39)
5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 30) (SEQ. ID NO: 40)
5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG 31) (SEQ. ID NO: 41)
5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG 32) (SEQ. ID NO: 42)
5'-GGC GGG CAC AGG CTG GGC-3' (FRAG 33) (SEQ. ID NO: 43)
5'-GC GGG CAC AGG CTG GGC-3' (FRAG 34) (SEQ. ID NO: 44)
5'-C GGG CAC AGG CTG GGC-3' (FRAG 35) (SEQ. ID NO: 45)
5'-GGG CAC AGG CTG GGC-3' (FRAG 36) (SEQ. ID NO: 46)
5'-GG CAC AGG CTG GGC-3' (FRAG 37) (SEQ. ID NO: 47)
5'-G CAC AGG CTG GGC-3' (FRAG 38) (SEQ. ID NO: 48)
5'-CAC AGG CTG GGC-3' (FRAG 39) (SEQ. ID NO: 49)
5'-AC AGG CTG GGC-3' (FRAG 40) (SEQ. ID NO: 50)
5'-C AGG CTG GGC-3' (FRAG 41) (SEQ. ID NO: 51)
5'-AGG CTG GGC-3' (FRAG 42) (SEQ. ID NO: 52)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3'(FRAG 43)(SEQ.ID NO:53)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 44)(SEQ.ID NO:54)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 45)(SEQ.ID NO:55)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 46)(SEQ.ID NO:56)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 47)(SEQ.ID NO:57)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 48)(SEQ. ID NO:58)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 49) (SEQ. ID NO: 59)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 50) (SEQ. ID NO: 60)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 51) (SEQ. ID NO: 61)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 52) (SEQ. ID NO: 62)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 53) (SEQ. ID NO: 63)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 54) (SEQ. ID NO: 64)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 55) (SEQ. ID NO: 65)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 56) (SEQ. ID NO: 66)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3'(FRAG 57) (SEQ. ID NO: 67)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 58) (SEQ. ID NO: 68)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 59) (SEQ. ID NO: 69)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 60) (SEQ. ID NO: 70)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 61) (SEQ. ID NO: 71)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 62) (SEQ. ID NO: 72)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 63) (SEQ. ID NO: 73)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 64) (SEQ. ID NO: 74)

5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 65) **(SEQ. ID NO: 75)**
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 66) **(SEQ. ID NO: 76)**
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 67) **(SEQ. ID NO: 77)**
5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) **(SEQ. ID NO: 78)**
5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) **(SEQ. ID NO: 79)**
5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) **(SEQ. ID NO: 80)**
5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) **(SEQ. ID NO: 81)**
5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) **(SEQ. ID NO: 82)**
5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) **(SEQ. ID NO: 83)**
5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) **(SEQ. ID NO: 84)**
5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) **(SEQ. ID NO: 85)**
5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) **(SEQ. ID NO: 86)**
5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) **(SEQ. ID NO: 87)**
5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) **(SEQ. ID NO: 88)**
5'-GGC GGC CTG GAA AGC-3' (FRAG 79) **(SEQ. ID NO: 89)**
5'-GGC GGC CTG GAA AG-3' (FRAG 80) **(SEQ. ID NO: 90)**
5'-GGC GGC CTG GAA A-3' (FRAG 81) **(SEQ. ID NO: 91)**
5'-GGC GGC CTG GAA-3' (FRAG 82) **(SEQ. ID NO: 92)**
5'-GGC GGC CTG GA-3' (FRAG 83) **(SEQ. ID NO: 93)**
5'-GGC GGC CTG G-3' (FRAG 84) **(SEQ. ID NO: 94)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 85) **(SEQ. ID NO: 95)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 86) **(SEQ. ID NO: 96)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 87) **(SEQ. ID NO: 97)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 88) **(SEQ. ID NO: 98)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 89) **(SEQ. ID NO: 99)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 90) **(SEQ. ID NO: 100)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 91) **(SEQ. ID NO: 101)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 92) **(SEQ. ID NO: 102)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 93) **(SEQ. ID NO: 103)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 94) **(SEQ. ID NO: 104)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 95) **(SEQ. ID NO: 105)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 96) **(SEQ. ID NO: 106)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 97) **(SEQ. ID NO: 107)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 98) **(SEQ. ID NO: 108)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 99) **(SEQ. ID NO: 109)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 100) **(SEQ. ID NO: 110)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) **(SEQ. ID NO: 111)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) **(SEQ. ID NO: 112)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) **(SEQ. ID NO: 113)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) **(SEQ. ID NO: 114)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) **(SEQ. ID NO: 115)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) **(SEQ. ID NO: 116)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) **(SEQ. ID NO: 117)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) **(SEQ. ID NO: 118)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) **(SEQ. ID NO: 119)**
5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) **(SEQ. ID NO: 120)**
5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) **(SEQ. ID NO: 121)**
5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) **(SEQ. ID NO: 122)**
5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) **(SEQ. ID NO: 123)**
5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) **(SEQ. ID NO: 124)**
5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) **(SEQ. ID NO: 125)**
5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) **(SEQ. ID NO: 126)**
5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) **(SEQ. ID NO: 127)**
5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) **(SEQ. ID NO: 128)**
5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) **(SEQ. ID NO: 129)**
5'-GC GGC CTG GAA AGC T-3' (FRAG 120) **(SEQ. ID NO: 130)**
5'-GC GGC CTG GAA AGC-3' (FRAG 121) **(SEQ. ID NO: 131)**
5'-GC GGC CTG GAA AG-3' (FRAG 122) **(SEQ. ID NO: 132)**
5'-GC GGC CTG GAA A-3' (FRAG 123) **(SEQ. ID NO: 133)**
5'-GC GGC CTG GAA-3' (FRAG 124) **(SEQ. ID NO: 134)**
5'-GC GGC CTG GA-3' (FRAG 125) **(SEQ. ID NO: 135)**

5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 126) **(SEQ. ID NO: 136)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 127) **(SEQ. ID NO: 137)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 128) **(SEQ. ID NO: 138)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 129) **(SEQ. ID NO: 139)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 130) **(SEQ. ID NO: 140)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 131) **(SEQ. ID NO: 141)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 132) **(SEQ. ID NO: 142)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 133) **(SEQ. ID NO: 143)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 134) **(SEQ. ID NO: 144)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 135) **(SEQ. ID NO: 145)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 136) **(SEQ. ID NO: 146)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) **(SEQ. ID NO: 147)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) **(SEQ. ID NO: 148)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) **(SEQ. ID NO: 149)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) **(SEQ. ID NO: 150)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) **(SEQ. ID NO: 151)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) **(SEQ. ID NO: 152)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRA 143) **(SEQ. ID NO: 153)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) **(SEQ. ID NO: 154)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) **(SEQ. ID NO: 155)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) **(SEQ. ID NO: 156)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) **(SEQ. ID NO: 157)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) **(SEQ. ID NO: 158)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 148) **(SEQ. ID NO: 159)**
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) **(SEQ. ID NO: 160)**
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) **(SEQ. ID NO: 161)**
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) **(SEQ. ID NO: 162)**
5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) **(SEQ. ID NO: 163)**
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) **(SEQ. ID NO: 164)**
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) **(SEQ. ID NO: 165)**
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) **(SEQ. ID NO: 166)**
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) **(SEQ. ID NO: 167)**
5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) **(SEQ. ID NO: 168)**
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) **(SEQ. ID NO: 169)**
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) **(SEQ. ID NO: 170)**
5'-C GGC CTG GAA AGC T-3' (FRAG 161) **(SEQ. ID NO: 171)**
5'-C GGC CTG GAA AGC-3' (FRAG 162) **(SEQ. ID NO: 172)**
5'-C GGC CTG GAA AG-3' (FRAG 163) **(SEQ. ID NO: 173)**
5'-C GGC CTG GAA A-3' (FRAG 164) **(SEQ. ID NO: 174)**
5'-C GGC CTG GAA-3' (FRAG 165) **(SEQ. ID NO: 175)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) **(SEQ. ID NO: 176)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) **(SEQ. ID NO: 177)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) **(SEQ. ID NO: 178)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 169) **(SEQ. ID NO: 179)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) **(SEQ. ID NO: 180)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) **(SEQ. ID NO: 181)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 172) **(SEQ. ID NO: 182)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 173) **(SEQ. ID NO: 183)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 174) **(SEQ. ID NO: 184)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 175) **(SEQ. ID NO: 185)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 176) **(SEQ. ID NO: 186)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 177) **(SEQ. ID NO: 187)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 178) **(SEQ. ID NO: 188)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 179) **(SEQ. ID NO: 189)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 180) **(SEQ. ID NO: 190)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 181) **(SEQ. ID NO: 191)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 182) **(SEQ. ID NO: 192)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 183) **(SEQ. ID NO: 193)**
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) **(SEQ. ID NO: 194)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) **(SEQ. ID NO: 195)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) **(SEQ. ID NO: 196)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) **(SEQ. ID NO: 197)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) **(SEQ. ID NO: 198)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) **(SEQ. ID NO: 199)**

5'- GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) **(SEQ. ID NO: 200)**

5'- GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) **(SEQ. ID NO: 201)**

5'- GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) **(SEQ. ID NO: 202)**

5'- GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) **(SEQ. ID NO: 203)**

5'- GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) **(SEQ. ID NO: 204)**

5'- GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) **(SEQ. ID NO: 205)**

5'- GGC CTG GAA AGC TGA GAT -3' (FRAG 196) **(SEQ. ID NO: 206)**

5'- GGC CTG GAA AGC TGA GA-3' (FRAG 197) **(SEQ. ID NO: 207)**

5'- GGC CTG GAA AGC TGA G-3' (FRAG 198) **(SEQ. ID NO: 208)**

5'- GGC CTG GAA AGC TGA-3' (FRAG 199) **(SEQ. ID NO: 209)**

5'- GGC CTG GAA AGC TG-3' (FRAG 200 **(SEQ. ID NO: 210)**

5'- GGC CTG GAA AGC T-3' (FRAG 201) **(SEQ. ID NO: 211)**

5'- GGC CTG GAA AGC-3' (FRAG 202) **(SEQ. ID NO: 212)**

5'- GGC CTG GAA AG-3' (FRAG 203) **(SEQ. ID NO: 213)**

5'- GGC CTG GAA A-3' (FRAG 204) **(SEQ. ID NO: 214)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 205) **(SEQ. ID NO: 215)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) **(SEQ. ID NO: 216)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) **(SEQ. ID NO: 217)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) **(SEQ. ID NO: 218)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) **(SEQ. ID NO: 219)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) **(SEQ. ID NO: 220)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) **(SEQ. ID NO: 221)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) **(SEQ. ID NO: 222)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) **(SEQ. ID NO: 223)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) **(SEQ. ID NO: 224)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) **(SEQ. ID NO: 225)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) **(SEQ. ID NO: 226)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) **(SEQ. ID NO: 227)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) **(SEQ. ID NO: 228)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) **(SEQ. ID NO: 229)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) **(SEQ. ID NO: 230)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) **(SEQ. ID NO: 231)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) **(SEQ. ID NO: 232)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) **(SEQ. ID NO: 233)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) **(SEQ. ID NO: 234)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) **(SEQ. ID NO: 235)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) **(SEQ. ID NO: 236)**

5'- GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) **(SEQ. ID NO: 237)**

5'- GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) **(SEQ. ID NO: 238)**

5'- GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) **(SEQ. ID NO: 239)**

5'- GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) **(SEQ. ID NO: 240)**

5'- GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) **(SEQ. ID NO: 241)**

5'- GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) **(SEQ. ID NO: 242)**

5'- GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) **(SEQ. ID NO: 243)**

5'- GC CTG GAA AGC TGA GAT G -3' (FRAG 234) **(SEQ. ID NO: 244)**

5'- GC CTG GAA AGC TGA GAT -3' (FRAG 235) **(SEQ. ID NO: 245)**

5'- GC CTG GAA AGC TGA GA-3' (FRAG 236) **(SEQ. ID NO: 246)**

5'- GC CTG GAA AGC TGA G-3' (FRAG 237) **(SEQ. ID NO: 247)**

5'- GC CTG GAA AGC TGA-3' (FRAG 238) **(SEQ. ID NO: 248)**

5'- GC CTG GAA AGC TG-3' (FRAG 239) **(SEQ. ID NO: 249)**

5'- GC CTG GAA AGC T-3' (FRAG 240) **(SEQ. ID NO: 250)**

5'- GC CTG GAA AGC-3' (FRAG 241) **(SEQ. ID NO: 251)**

5'- GC CTG GAA AG-3' (FRAG 242) **(SEQ. ID NO: 252)**

5'- C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) **(SEQ. ID NO: 253)**

5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) **(SEQ. ID NO: 254)**

5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) **(SEQ. ID NO: 255)**

5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) **(SEQ. ID NO: 256)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) **(SEQ. ID NO: 257)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) **(SEQ. ID NO: 258)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) **(SEQ. ID NO: 259)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) **(SEQ. ID NO: 260)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) **(SEQ. ID NO: 261)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 252) **(SEQ. ID NO: 262)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) **(SEQ. ID NO: 263)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) **(SEQ. ID NO: 264)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) **(SEQ. ID NO: 265)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) **(SEQ. ID NO: 266)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) **(SEQ. ID NO: 267)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 258) **(SEQ. ID NO: 268)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 259) **(SEQ. ID NO: 269)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 260) **(SEQ. ID NO: 270)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 261) **(SEQ. ID NO: 271)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 262) **(SEQ. ID NO: 272)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 263) **(SEQ. ID NO: 273)**
5'- C CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 264) **(SEQ. ID NO: 274)**
5'- C CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 265) **(SEQ. ID NO: 275)**
5'- C CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 266) **(SEQ. ID NO: 276)**
5'- C CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 267) **(SEQ. ID NO: 277)**
5'- C CTG GAA AGC TGA GAT GGA GG -3' (FRAG 268) **(SEQ. ID NO: 278)**
5'- C CTG GAA AGC TGA GAT GGA G -3' (FRAG 269) **(SEQ. ID NO: 279)**
5'- C CTG GAA AGC TGA GAT GGA -3' (FRAG 270) **(SEQ. ID NO: 280)**
5'- C CTG GAA AGC TGA GAT GG -3' (FRAG 271) **(SEQ. ID NO: 281)**
5'- C CTG GAA AGC TGA GAT G -3' (FRAG 272) **(SEQ. ID NO: 282)**
5'- C CTG GAA AGC TGA GAT -3' (FRAG 273) **(SEQ. ID NO: 283)**
5'- C CTG GAA AGC TGA GA-3' (FRAG 274) **(SEQ. ID NO: 284)**
5'- C CTG GAA AGC TGA G-3' (FRAG 275) **(SEQ. ID NO: 285)**
5'- C CTG GAA AGC TGA-3' (FRAG 276) **(SEQ. ID NO: 286)**
5'- C CTG GAA AGC TG-3' (FRAG 277) **(SEQ. ID NO: 287)**
5'- C CTG GAA AGC T 3' (FRAG 278) **(SEQ. ID NO: 288)**
5'- C CTG GAA AGC-3' (FRAG 279) **(SEQ. ID NO: 289)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 280) **(SEQ. ID NO: 290)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 281) **(SEQ. ID NO: 291)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 282) **(SEQ. ID NO: 292)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) **(SEQ. ID NO: 293)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 284) **(SEQ. ID NO: 294)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 285) **(SEQ. ID NO: 295)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) **(SEQ. ID NO: 296)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 287) **(SEQ. ID NO: 297)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 288) **(SEQ. ID NO: 298)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 289) **(SEQ. ID NO: 299)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 290) **(SEQ. ID NO: 300)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 291) **(SEQ. ID NO: 301)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) **(SEQ. ID NO: 302)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 293) **(SEQ. ID NO: 303)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 294) **(SEQ. ID NO: 304)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) **(SEQ. ID NO: 305)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) **(SEQ. ID NO: 306)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) **(SEQ. ID NO: 307)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) **(SEQ. ID NO: 308)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 299) **(SEQ. ID NO: 309)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 300) **(SEQ. ID NO: 310)**
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) **(SEQ. ID NO: 311)**
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) **(SEQ. ID NO: 312)**
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) **(SEQ. ID NO: 313)**
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) **(SEQ. ID NO: 314)**
5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) **(SEQ. ID NO: 315)**
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) **(SEQ. ID NO: 316)**
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) **(SEQ. ID NO: 317)**

5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) **(SEQ. ID NO: 318)**
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) **(SEQ. ID NO: 319)**
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) **(SEQ. ID NO: 320)**
5'- CTG GAA AGC TGA GA-3' (FRAG 311) **(SEQ. ID NO: 321)**
5'- CTG GAA AGC TGA G-3' (FRAG 312) **(SEQ. ID NO: 322)**
5'- CTG GAA AGC TGA-3' (FRAG 313) **(SEQ. ID NO: 323)**
5'- CTG GAA AGC TG 3' (FRAG 314) **(SEQ. ID NO: 324)**
5'- CTG GAA AGC T-3' (FRAG 315) **(SEQ. ID NO: 325)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 316) **(SEQ. ID NO: 326)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 317) **(SEQ. ID NO: 327)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 318) **(SEQ. ID NO: 328)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) **(SEQ. ID NO: 329)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 320) **(SEQ. ID NO: 330)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 321) **(SEQ. ID NO: 331)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) **(SEQ. ID NO: 332)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 323) **(SEQ. ID NO: 333)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 324) **(SEQ. ID NO: 334)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 325) **(SEQ. ID NO: 335)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 326) **(SEQ. ID NO: 336)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 327) **(SEQ. ID NO: 337)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) **(SEQ. ID NO: 338)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 329) **(SEQ. ID NO: 339)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 330) **(SEQ. ID NO: 340)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) **(SEQ. ID NO: 341)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) **(SEQ. ID NO: 342)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) **(SEQ. ID NO: 343)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) **(SEQ. ID NO: 344)**
5'- TG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 335) **(SEQ. ID NO: 345)**
5'- TG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 336) **(SEQ. ID NO: 346)**
5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) **(SEQ. ID NO: 347)**
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) **(SEQ. ID NO: 348)**
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) **(SEQ. ID NO: 349)**
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) **(SEQ. ID NO: 350)**
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) **(SEQ. ID NO: 351)**
5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) **(SEQ. ID NO: 352)**
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) **(SEQ. ID NO: 353)**
5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) **(SEQ. ID NO: 354)**
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) **(SEQ. ID NO: 355)**
5'- TG GAA AGC TGA GAT -3' (FRAG 346) **(SEQ. ID NO: 356)**
5'- TG GAA AGC TGA GA-3' (FRAG 347) **(SEQ. ID NO: 357)**
5'- TG GAA AGC TGA G-3' (FRAG 348) **(SEQ. ID NO: 358)**
5'- TG GAA AGC TGA 3' (FRAG 349) **(SEQ. ID NO: 359)**
5'- TG GAA AGC TG-3 (FRAG 350) **(SEQ. ID NO: 360)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) **(SEQ. ID NO: 361)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) **(SEQ. ID NO: 362)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) **(SEQ. ID NO: 363)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) **(SEQ. ID NO: 364)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) **(SEQ. ID NO: 365)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) **(SEQ. ID NO: 366)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) **(SEQ. ID NO: 367)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) **(SEQ. ID NO: 368)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) **(SEQ. ID NO: 369)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) **(SEQ. ID NO: 370)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) **(SEQ. ID NO: 371)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) **(SEQ. ID NO: 372)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) **(SEQ. ID NO: 373)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 364) **(SEQ. ID NO: 374)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 365) **(SEQ. ID NO: 375)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 366) **(SEQ. ID NO: 376)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 367) **(SEQ. ID NO: 377)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 368) **(SEQ. ID NO: 378)**
5'- G GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 369) **(SEQ. ID NO: 379)**

5'- G GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 370) **(SEQ. ID NO: 380)**
5'- G GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 371) **(SEQ. ID NO: 381)**
5'- G GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 372) **(SEQ. ID NO: 382)**
5'- G GAA AGC TGA GAT GGA GGG CG -3' (FRAG 373) **(SEQ. ID NO: 383)**
5'- G GAA AGC TGA GAT GGA GGG C -3' (FRAG 374) **(SEQ. ID NO: 384)**
5'- G GAA AGC TGA GAT GGA GGG -3' (FRAG 375) **(SEQ. ID NO: 385)**
5'- G GAA AGC TGA GAT GGA GG -3' (FRAG 376) **(SEQ. ID NO: 386)**
5'- G GAA AGC TGA GAT GGA G -3' (FRAG 377) **(SEQ. ID NO: 387)**
5'- G GAA AGC TGA GAT GGA -3' (FRAG 378) **(SEQ. ID NO: 388)**
5'- G GAA AGC TGA GAT GG -3' (FRAG 379) **(SEQ. ID NO: 389)**
5'- G GAA AGC TGA GAT G -3' (FRAG 380) **(SEQ. ID NO: 390)**
5'- G GAA AGC TGA GAT -3' (FRAG 381) **(SEQ. ID NO: 391)**
5'- G GAA AGC TGA GA-3' (FRAG 382) **(SEQ. ID NO: 392)**
5'- G GAA AGC TGA G-3' (FRAG 383) **(SEQ. ID NO: 393)**
5'- G GAA AGC TGA-3' (FRAG 384) **(SEQ. ID NO: 394)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) **(SEQ. ID NO: 395)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) **(SEQ. ID NO: 396)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) **(SEQ. ID NO: 397)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) **(SEQ. ID NO: 398)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) **(SEQ. ID NO: 399)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) **(SEQ. ID NO: 400)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) **(SEQ. ID NO: 401)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) **(SEQ. ID NO: 402)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) **(SEQ. ID NO: 403)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) **(SEQ. ID NO: 404)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) **(SEQ. ID NO: 405)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 396) **(SEQ. ID NO: 406)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 397) **(SEQ. ID NO: 407)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 398) **(SEQ. ID NO: 408)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 399) **(SEQ. ID NO: 409)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 400) **(SEQ. ID NO: 410)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 401) **(SEQ. ID NO: 411)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 402) **(SEQ. ID NO: 412)**
5'- GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 403) **(SEQ. ID NO: 413)**
5'- GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 404) **(SEQ. ID NO: 414)**
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 405) **(SEQ. ID NO: 415)**
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 406) **(SEQ. ID NO: 416)**
5'- GAA AGC TGA GAT GGA GGG CG -3' (FRAG 407) **(SEQ. ID NO: 417)**
5'- GAA AGC TGA GAT GGA GGG C -3' (FRAG 408) **(SEQ. ID NO: 418)**
5'- GAA AGC TGA GAT GGA GGG -3' (FRAG 409) **(SEQ. ID NO: 419)**
5'- GAA AGC TGA GAT GGA GG -3' (FRAG 410) **(SEQ. ID NO: 420)**
5'- GAA AGC TGA GAT GGA G -3' (FRAG 411) **(SEQ. ID NO: 421)**
5'- GAA AGC TGA GAT GGA -3' (FRAG 412) **(SEQ. ID NO: 422)**
5'- GAA AGC TGA GAT GG -3' (FRAG 413) **(SEQ. ID NO: 423)**
5'- GAA AGC TGA GAT G -3' (FRAG 414) **(SEQ. ID NO: 424)**
5'- GAA AGC TGA GAT -3' (FRAG 415) **(SEQ. ID NO: 425)**
5'- GAA AGC TGA GA-3' (FRAG 416) **(SEQ. ID NO: 426)**
5'- GAA AGC TGA G-3' (FRAG 417) **(SEQ. ID NO: 427)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) **(SEQ. ID NO: 428)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) **(SEQ. ID NO: 429)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) **(SEQ. ID NO: 430)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) **(SEQ. ID NO: 431)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) **(SEQ. ID NO: 432)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) **(SEQ. ID NO: 433)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3'(FRAG 424) **(SEQ. ID NO: 434)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) **(SEQ. ID NO: 435)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) **(SEQ. ID NO: 436)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) **(SEQ. ID NO: 437)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) **(SEQ. ID NO: 438)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) **(SEQ. ID NO: 439)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) **(SEQ. ID NO: 440)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 431) **(SEQ. ID NO: 441)**

5'- AA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 432) **(SEQ. ID NO: 442)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 433) **(SEQ. ID NO: 443)**
5'- AA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 434) **(SEQ. ID NO: 444)**
5'- AA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 435) **(SEQ. ID NO: 445)**
5'- AA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 436) **(SEQ. ID NO: 446)**
5'- AA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 437) **(SEQ. ID NO: 447)**
5'- AA AGC TGA GAT GGA GGG CGG C-3' (FRAG 438) **(SEQ. ID NO: 448)**
5'- AA AGC TGA GAT GGA GGG CGG -3' (FRAG 439) **(SEQ. ID NO: 449)**
5'- AA AGC TGA GAT GGA GGG CG -3' (FRAG 440) **(SEQ. ID NO: 450)**
5'- AA AGC TGA GAT GGA GGG C -3' (FRAG 441) **(SEQ. ID NO: 451)**
5'- AA AGC TGA GAT GGA GGG -3' (FRAG 442) **(SEQ. ID NO: 452)**
5'- AA AGC TGA GAT GGA GG -3' (FRAG 443) **(SEQ. ID NO: 453)**
5'- AA AGC TGA GAT GGA G -3' (FRAG 444) **(SEQ. ID NO: 454)**
5'- AA AGC TGA GAT GGA -3' (FRAG 445) **(SEQ. ID NO: 455)**
5'- AA AGC TGA GAT GG -3' (FRAG 446) **(SEQ. ID NO: 456)**
5'- AA AGC TGA GAT G -3' (FRAG 447) **(SEQ. ID NO: 457)**
5'- AA AGC TGA GAT -3' (FRAG 448) **(SEQ. ID NO: 458)**
5'- AA AGC TGA GA-3' (FRAG 449) **(SEQ. ID NO: 459)**
5'- A AGC TGA GAT GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) **(SEQ. ID NO: 460)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) **(SEQ. ID NO: 461)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) **(SEQ. ID NO: 462)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) **(SEQ. ID NO: 463)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 454) **(SEQ. ID NO: 464)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) **(SEQ. ID NO: 465)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) **(SEQ. ID NO: 466)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 457) **(SEQ. ID NO: 467)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) **(SEQ. ID NO: 468)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) **(SEQ. ID NO: 469)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) **(SEQ. ID NO: 470)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 461) **(SEQ. ID NO: 471)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 462) **(SEQ. ID NO: 472)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 463) **(SEQ. ID NO: 473)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 464) **(SEQ. ID NO: 474)**
5'- A AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 465) **(SEQ. ID NO: 475)**
5'- A AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 466) **(SEQ. ID NO: 476)**
5'- A AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 467) **(SEQ. ID NO: 477)**
5'- A AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 468) **(SEQ. ID NO: 478)**
5'- A AGC TGA GAT GGA GGG CGG CA-3' (FRAG 469) **(SEQ. ID NO: 479)**
5'- A AGC TGA GAT GGA GGG CGG C-3' (FRAG 470) **(SEQ. ID NO: 480)**
5'- A AGC TGA GAT GGA GGG CGG -3' (FRAG 471) **(SEQ. ID NO: 481)**
5'- A AGC TGA GAT GGA GGG CG -3' (FRAG 472) **(SEQ. ID NO: 482)**
5'- A AGC TGA GAT GGA GGG C -3' (FRAG 473) **(SEQ. ID NO: 483)**
5'- A AGC TGA GAT GGA GGG -3' (FRAG 474) **(SEQ. ID NO: 484)**
5'- A AGC TGA GAT GGA GG -3' (FRAG 475) **(SEQ. ID NO: 485)**
5'- A AGC TGA GAT GGA G -3' (FRAG 476) **(SEQ. ID NO: 486)**
5'- A AGC TGA GAT GGA -3' (FRAG 477) **(SEQ. ID NO: 487)**
5'- A AGC TGA GAT GG -3' (FRAG 478) **(SEQ. ID NO: 488)**
5'- A AGC TGA GAT G -3' (FRAG 479) **(SEQ. ID NO: 489)**
5'- A AGC TGA GAT -3' (FRAG 480) **(SEQ. ID NO: 490)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 481) **(SEQ. ID NO: 491)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) **(SEQ. ID NO: 492)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) **(SEQ. ID NO: 493)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) **(SEQ. ID NO: 494)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 485) **(SEQ. ID NO: 495)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) **(SEQ. ID NO: 496)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) **(SEQ. ID NO: 497)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 488) **(SEQ. ID NO: 498)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) **(SEQ. ID NO: 499)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 490) **(SEQ. ID NO: 500)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) **(SEQ. ID NO: 501)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 492) **(SEQ. ID NO: 502)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 493) **(SEQ. ID NO: 503)**

5'- AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 494) **(SEQ. ID NO: 504)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 495) **(SEQ. ID NO: 505)**
5'- AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 496) **(SEQ. ID NO: 506)**
5'- AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 497) **(SEQ. ID NO: 507)**
5'- AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 498) **(SEQ. ID NO: 508)**
5'- AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 499) **(SEQ. ID NO: 509)**
5'- AGC TGA GAT GGA GGG CGG CA-3' (FRAG 500) **(SEQ. ID NO: 510)**
5'- AGC TGA GAT GGA GGG CGG C-3' (FRAG 501) **(SEQ. ID NO: 511)**
5'- AGC TGA GAT GGA GGG CGG -3' (FRAG 502) **(SEQ. ID NO: 512)**
5'- AGC TGA GAT GGA GGG CG -3' (FRAG 503) **(SEQ. ID NO: 513)**
5'- AGC TGA GAT GGA GGG C -3' (FRAG 504) **(SEQ. ID NO: 514)**
5'- AGC TGA GAT GGA GGG -3' (FRAG 505) **(SEQ. ID NO: 515)**
5'- AGC TGA GAT GGA GG -3' (FRAG 506) **(SEQ. ID NO: 516)**
5'- AGC TGA GAT GGA G -3' (FRAG 507) **(SEQ. ID NO: 517)**
5'- AGC TGA GAT GGA -3' (FRAG 508) **(SEQ. ID NO: 518)**
5'- AGC TGA GAT GG -3' (FRAG 509) **(SEQ. ID NO: 519)**
5'- AGC TGA GAT G -3' (FRAG 510) **(SEQ. ID NO: 520)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) **(SEQ. ID NO: 521)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) **(SEQ. ID NO: 522)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) **(SEQ. ID NO: 523)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) **(SEQ. ID NO: 524)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) **(SEQ. ID NO: 525)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) **(SEQ. ID NO: 526)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) **(SEQ. ID NO: 527)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) **(SEQ. ID NO: 528)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) **(SEQ. ID NO: 529)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 520) **(SEQ. ID NO: 530)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 521) **(SEQ. ID NO: 531)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 522) **(SEQ. ID NO: 532)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 523) **(SEQ. ID NO: 533)**
5'- GC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 524) **(SEQ. ID NO: 534)**
5'- GC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 525) **(SEQ. ID NO: 535)**
5'- GC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 526) **(SEQ. ID NO: 536)**
5'- GC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 527) **(SEQ. ID NO: 537)**
5'- GC TGA GAT GGA GGG CGG CAT G -3' (FRAG 528) **(SEQ. ID NO: 538)**
5'- GC TGA GAT GGA GGG CGG CAT -3' (FRAG 529) **(SEQ. ID NO: 539)**
5'- GC TGA GAT GGA GGG CGG CA-3' (FRAG 530) **(SEQ. ID NO: 540)**
5'- GC TGA GAT GGA GGG CGG C-3' (FRAG 531) **(SEQ. ID NO: 541)**
5'- GC TGA GAT GGA GGG CGG -3' (FRAG 532) **(SEQ. ID NO: 542)**
5'- GC TGA GAT GGA GGG CG -3' (FRAG 533) **(SEQ. ID NO: 543)**
5'- GC TGA GAT GGA GGG C -3' (FRAG 534) **(SEQ. ID NO: 544)**
5'- GC TGA GAT GGA GGG -3' (FRAG 535) **(SEQ. ID NO: 545)**
5'- GC TGA GAT GGA GG -3' (FRAG 536) **(SEQ. ID NO: 546)**
5'- GC TGA GAT GGA G -3' (FRAG 537) **(SEQ. ID NO: 547)**
5'- GC TGA GAT GGA -3' (FRAG 538) **(SEQ. ID NO: 548)**
5'- GC TGA GAT GG -3' (FRAG 539) **(SEQ. ID NO: 549)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) **(SEQ. ID NO: 550)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) **(SEQ. ID NO: 551)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) **(SEQ. ID NO: 552)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) **(SEQ. ID NO: 553)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) **(SEQ. ID NO: 554)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) **(SEQ. ID NO: 555)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) **(SEQ. ID NO: 556)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) **(SEQ. ID NO: 557)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) **(SEQ. ID NO: 558)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 549) **(SEQ. ID NO: 559)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 550) **(SEQ. ID NO: 560)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 551) **(SEQ. ID NO: 561)**
5'- C TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 552) **(SEQ. ID NO: 562)**
5'- C TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 553) **(SEQ. ID NO: 563)**
5'- C TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 554) **(SEQ. ID NO: 564)**
5'- C TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 555) **(SEQ. ID NO: 565)**

5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) **(SEQ. ID NO: 566)**
5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) **(SEQ. ID NO: 567)**
5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) **(SEQ. ID NO: 568)**
5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) **(SEQ. ID NO: 569)**
5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) **(SEQ. ID NO: 570)**
5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) **(SEQ. ID NO: 571)**
5'- C TGA GAT GGA GGG CG -3' (FRAG 562) **(SEQ. ID NO: 572)**
5'- C TGA GAT GGA GGG C -3' (FRAG 563) **(SEQ. ID NO: 573)**
5'- C TGA GAT GGA GGG -3' (FRAG 564) **(SEQ. ID NO: 574)**
5'- C TGA GAT GGA GG -3' (FRAG 565) **(SEQ. ID NO: 575)**
5'- C TGA GAT GGA G -3' (FRAG 566) **(SEQ. ID NO: 576)**
5'- C TGA GAT GGA -3' (FRAG 567) **(SEQ. ID NO: 577)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) **(SEQ. ID NO: 578)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) **(SEQ. ID NO: 579)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) **(SEQ. ID NO: 580)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) **(SEQ. ID NO: 581)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) **(SEQ. ID NO: 582)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) **(SEQ. ID NO: 583)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) **(SEQ. ID NO: 584)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) **(SEQ. ID NO: 585)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) **(SEQ. ID NO: 586)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) **(SEQ. ID NO: 587)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) **(SEQ. ID NO: 588)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) **(SEQ. ID NO: 589)**
5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) **(SEQ. ID NO: 590)**
5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) **(SEQ. ID NO: 591)**
5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) **(SEQ. ID NO: 592)**
5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) **(SEQ. ID NO: 593)**
5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) **(SEQ. ID NO: 594)**
5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) **(SEQ. ID NO: 595)**
5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) **(SEQ. ID NO: 596)**
5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) **(SEQ. ID NO: 597)**
5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) **(SEQ. ID NO: 598)**
5'- TGA GAT GGA GGG CGG -3' (FRAG 589) **(SEQ. ID NO: 599)**
5'- TGA GAT GGA GGG CG -3' (FRAG 590) **(SEQ. ID NO: 600)**
5'- TGA GAT GGA GGG C -3' (FRAG 591) **(SEQ. ID NO: 601)**
5'- TGA GAT GGA GGG -3' (FRAG 592) **(SEQ. ID NO: 602)**
5'- TGA GAT GGA GG -3' (FRAG 593) **(SEQ. ID NO: 603)**
5'- TGA GAT GGA G -3' (FRAG 594) **(SEQ. ID NO: 604)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) **(SEQ. ID NO: 605)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) **(SEQ. ID NO: 606)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) **(SEQ. ID NO: 607)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) **(SEQ. ID NO: 608)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) **(SEQ. ID NO: 609)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) **(SEQ. ID NO: 610)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) **(SEQ. ID NO: 611)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AG-3' (FRAG 602) **(SEQ. ID NO: 612)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC A-3' (FRAG 603) **(SEQ. ID NO: 613)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CAC-3' (FRAG 604) **(SEQ. ID NO: 614)**
5'- GA GAT GGA GCG CGG CAT GGC GGG CA-3' (FRAG 605) **(SEQ. ID NO: 615)**
5'- GA GAT GGA GCG CGG CAT GGC GGG C-3' (FRAG 606) **(SEQ. ID NO: 616)**
5'- GA GAT GGA GCG CGG CAT GGC GGG -3' (FRAG 607) **(SEQ. ID NO: 617)**
5'- GA GAT GGA GCG CGG CAT GGC GG-3' (FRAG 608) **(SEQ. ID NO: 618)**
5'- GA GAT GGA GCG CGG CAT GGC G-3' (FRAG 609) **(SEQ. ID NO: 619)**
5'- GA GAT GGA GCG CGG CAT GGC -3' (FRAG 610) **(SEQ. ID NO: 620)**
5'- GA GAT GGA GCG CGG CAT GG -3' (FRAG 611) **(SEQ. ID NO: 621)**
5'- GA GAT GGA GCG CGG CAT G -3' (FRAG 612) **(SEQ. ID NO: 622)**
5'- GA GAT GGA GCG CGG CAT -3' (FRAG 613) **(SEQ. ID NO: 623)**
5'- GA GAT GGA GCG CGG CA-3' (FRAG 614) **(SEQ. ID NO: 624)**
5'- GA GAT GGA GCG CGG C-3' (FRAG 615) **(SEQ. ID NO: 625)**
5'- GA GAT GGA GCG CGG -3' (FRAG 616) **(SEQ. ID NO: 626)**
5'- GA GAT GGA GCG CG -3' (FRAG 617) **(SEQ. ID NO: 627)**

5'- GA GAT GGA GGG C -3' (FRAG 618) **(SEQ. ID NO: 628)**
5'- GA GAT GGA GGG -3' (FRAG 619) **(SEQ. ID NO: 629)**
5'- GA GAT GGA GG -3' (FRAG 620) **(SEQ. ID NO: 630)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) **(SEQ. ID NO: 631)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) **(SEQ. ID NO: 632)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) **(SEQ. ID NO: 633)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) **(SEQ. ID NO: 634)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) **(SEQ. ID NO: 635)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) **(SEQ. ID NO: 636)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 627) **(SEQ. ID NO: 637)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 628) **(SEQ. ID NO: 638)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 629) **(SEQ. ID NO: 639)**
5'- A GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 630) **(SEQ. ID NO: 640)**
5'- A GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 631) **(SEQ. ID NO: 641)**
5'- A GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 632) **(SEQ. ID NO: 642)**
5'- A GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 633) **(SEQ. ID NO: 643)**
5'- A GAT GGA GGG CGG CAT GGC GG-3' (FRAG 634) **(SEQ. ID NO: 644)**
5'- A GAT GGA GGG CGG CAT GGC G-3' (FRAG 635) **(SEQ. ID NO: 645)**
5'- A GAT GGA GGG CGG CAT GGC -3' (FRAG 636) **(SEQ. ID NO: 646)**
5'- A GAT GGA GGG CGG CAT GG -3' (FRAG 637) **(SEQ. ID NO: 647)**
5'- A GAT GGA GGG CGG CAT G -3' (FRAG 638) **(SEQ. ID NO: 648)**
5'- A GAT GGA GGG CGG CAT -3' (FRAG 639) **(SEQ. ID NO: 649)**
5'- A GAT GGA GGG CGG CA-3' (FRAG 640) **(SEQ. ID NO: 650)**
5'- A GAT GGA GGG CGG C-3' (FRAG 641) **(SEQ. ID NO: 651)**
5'- A GAT GGA GGG CGG -3' (FRAG 642) **(SEQ. ID NO: 652)**
5'- A GAT GGA GGG CG -3' (FRAG 643) **(SEQ. ID NO: 653)**
5'- A GAT GGA GGG C -3' (FRAG 644) **(SEQ. ID NO: 654)**
5'- A GAT GGA GGG -3' (FRAG 645) **(SEQ. ID NO: 655)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) **(SEQ. ID NO: 656)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) **(SEQ. ID NO: 657)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) **(SEQ. ID NO: 658)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 6) **(SEQ. ID NO: 659)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) **(SEQ. ID NO: 660)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) **(SEQ. ID NO: 661)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) **(SEQ. ID NO: 662)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) **(SEQ. ID NO: 663)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) **(SEQ. ID NO: 664)**
5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) **(SEQ. ID NO: 665)**
5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) **(SEQ. ID NO: 666)**
5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) **(SEQ. ID NO: 667)**
5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) **(SEQ. ID NO: 668)**
5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) **(SEQ. ID NO: 669)**
5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) **(SEQ. ID NO: 670)**
5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) **(SEQ. ID NO: 671)**
5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) **(SEQ. ID NO: 672)**
5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) **(SEQ. ID NO: 673)**
5'- GAT GGA GGG CGG CAT -3' (FRAG 664) **(SEQ. ID NO: 674)**
5'- GAT GGA GGG CGG CA-3' (FRAG 665) **(SEQ. ID NO: 675)**
5'- GAT GGA GGG CGG C-3' (FRAG 666) **(SEQ. ID NO: 676)**
5'- GAT GGA GGG CGG -3' (FRAG 667) **(SEQ. ID NO: 677)**
5'- GAT GGA GGG CG -3' (FRAG 668) **(SEQ. ID NO: 678)**
5'- GAT GGA GGG C -3' (FRAG 669) **(SEQ. ID NO: 679)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) **(SEQ. ID NO: 680)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) **(SEQ. ID NO: 681)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) **(SEQ. ID NO: 682)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) **(SEQ. ID NO: 683)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 674) **(SEQ. ID NO: 684)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 675) **(SEQ. ID NO: 685)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 676) **(SEQ. ID NO: 686)**
5'- AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 677) **(SEQ. ID NO: 687)**
5'- AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 678) **(SEQ. ID NO: 688)**
5'- AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 679) **(SEQ. ID NO: 689)**

5'- AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 680) **(SEQ. ID NO: 690)**
5'- AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 681) **(SEQ. ID NO: 691)**
5'- AT GGA GGG CGG CAT GGC GGG -3' (FRAG 682) **(SEQ. ID NO: 692)**
5'- AT GGA GGG CGG CAT GGC GG-3' (FRAG 683) **(SEQ. ID NO: 693)**
5'- AT GGA GGG CGG CAT GGC G-3' (FRAG 684) **(SEQ. ID NO: 694)**
5'- AT GGA GGG CGG CAT GGC -3' (FRAG 685) **(SEQ. ID NO: 695)**
5'- AT GGA GGG CGG CAT GG -3' (FRAG 686) **(SEQ. ID NO: 696)**
5'- AT GGA GGG CGG CAT G -3' (FRAG 687) **(SEQ. ID NO: 697)**
5'- AT GGA GGG CGG CAT -3' (FRAG 688) **(SEQ. ID NO: 698)**
5'- AT GGA GGG CGG CA-3' (FRAG 689) **(SEQ. ID NO: 699)**
5'- AT GGA GGG CGG C-3' (FRAG 690) **(SEQ. ID NO: 700)**
5'- AT GGA GGG CGG -3' (FRAG 691) **(SEQ. ID NO: 701)**
5'- AT GGA GGG CG -3' (FRAG 692) **(SEQ. ID NO: 702)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) **(SEQ. ID NO: 703)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) **(SEQ. ID NO: 704)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) **(SEQ. ID NO: 705)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) **(SEQ. ID NO: 706)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 697) **(SEQ. ID NO: 707)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 698) **(SEQ. ID NO: 708)**
5'- T GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 699) **(SEQ. ID NO: 709)**
5'- T GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 700) **(SEQ. ID NO: 710)**
5'- T GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 701) **(SEQ. ID NO: 711)**
5'- T GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 702) **(SEQ. ID NO: 712)**
5'- T GGA GGG CGG CAT GGC GGG CA-3' (FRAG 703) **(SEQ. ID NO: 713)**
5'- T GGA GGG CGG CAT GGC GGG C-3' (FRAG 704) **(SEQ. ID NO: 714)**
5'- T GGA GGG CGG CAT GGC GGG -3' (FRAG 705) **(SEQ. ID NO: 715)**
5'- T GGA GGG CGG CAT GGC GG-3' (FRAG 706) **(SEQ. ID NO: 716)**
5'- T GGA GGG CGG CAT GGC G-3' (FRAG 707) **(SEQ. ID NO: 717)**
5'- T GGA GGG CGG CAT GGC -3' (FRAG 708) **(SEQ. ID NO: 718)**
5'- T GGA GGG CGG CAT GG -3' (FRAG 709) **(SEQ. ID NO: 719)**
5'- T GGA GGG CGG CAT G -3' (FRAG 710) **(SEQ. ID NO: 720)**
5'- T GGA GGG CGG CAT -3' (FRAG 711) **(SEQ. ID NO: 721)**
5'- T GGA GGG CGG CA-3' (FRAG 712) **(SEQ. ID NO: 722)**
5'- T GGA GGG CGG C-3' (FRAG 713) **(SEQ. ID NO: 723)**
5'- T GGA GGG CGG -3' (FRAG 714) **(SEQ. ID NO: 724)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) **(SEQ. ID NO: 725)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) **(SEQ. ID NO: 726)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) **(SEQ. ID NO: 727)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 718) **(SEQ. ID NO: 728)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 719) **(SEQ. ID NO: 729)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 720) **(SEQ. ID NO: 730)**
5'- GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 721) **(SEQ. ID NO: 731)**
5'- GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 722) **(SEQ. ID NO: 732)**
5'- GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 723) **(SEQ. ID NO: 733)**
5'- GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 724) **(SEQ. ID NO: 734)**
5'- GGA GGG CGG CAT GGC GGG CA-3' (FRAG 725) **(SEQ. ID NO: 735)**
5'- GGA GGG CGG CAT GGC GGG C-3' (FRAG 726) **(SEQ. ID NO: 736)**
5'- GGA GGG CGG CAT GGC GGG -3' (FRAG 727) **(SEQ. ID NO: 737)**
5'- GGA GGG CGG CAT GGC GG-3' (FRAG 728) **(SEQ. ID NO: 738)**
5'- GGA GGG CGG CAT GGC G-3' (FRAG 729) **(SEQ. ID NO: 739)**
5'- GGA GGG CGG CAT GGC -3' (FRAG 730) **(SEQ. ID NO: 740)**
5'- GGA GGG CGG CAT GG -3' (FRAG 731) **(SEQ. ID NO: 741)**
5'- GGA GGG CGG CAT G -3' (FRAG 732) **(SEQ. ID NO: 742)**
5'- GGA GGG CGG CAT -3' (FRAG 733) **(SEQ. ID NO: 743)**
5'- GGA GGG CGG CA-3' (FRAG 734) **(SEQ. ID NO: 744)**
5'- GGA GGG CGG C-3' (FRAG 735) **(SEQ. ID NO: 745)**
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) **(SEQ. ID NO: 746)**
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) **(SEQ. ID NO: 747)**
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) **(SEQ. ID NO: 748)**
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) **(SEQ. ID NO: 749)**
5'- GA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 740) **(SEQ. ID NO: 750)**
5'- GA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 741) **(SEQ. ID NO: 751)**

5'- GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) **(SEQ. ID NO: 752)**
5'- GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) **(SEQ. ID NO: 753)**
5'- GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) **(SEQ. ID NO: 754)**
5'- GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) **(SEQ. ID NO: 755)**
5'- GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) **(SEQ. ID NO: 756)**
5'- GA GGG CGG CAT GGC GGG C-3' (FRAG 747) **(SEQ. ID NO: 757)**
5'- GA GGG CGG CAT GGC GGG -3' (FRAG 748) **(SEQ. ID NO: 758)**
5'- GA GGG CGG CAT GGC GG-3' (FRAG 749) **(SEQ. ID NO: 759)**
5'- GA GGG CGG CAT GGC G-3' (FRAG 750) **(SEQ. ID NO: 760)**
5'- GA GGG CGG CAT GGC -3' (FRAG 751) **(SEQ. ID NO: 761)**
5'- GA GGG CGG CAT GG -3' (FRAG 752) **(SEQ. ID NO: 762)**
5'- GA GGG CGG CAT G -3' (FRAG 753) **(SEQ. ID NO: 763)**
5'- GA GGG CGG CAT -3' (FRAG 754) **(SEQ. ID NO: 764)**
5'- GA GGG CGG CA-3' (FRAG 755) **(SEQ. ID NO: 765)**
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 756) **(SEQ. ID NO: 766)**
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 757) **(SEQ. ID NO: 767)**
5'- A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 758) **(SEQ. ID NO: 768)**
5'- A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 759) **(SEQ. ID NO: 769)**
5'- A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 760) **(SEQ. ID NO: 770)**
5'- A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 761) **(SEQ. ID NO: 771)**
5'- A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 762) **(SEQ. ID NO: 772)**
5'- A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 763) **(SEQ. ID NO: 773)**
5'- A GGG CGG CAT GGC GGG CAC A-3' (FRAG 764) **(SEQ. ID NO: 774)**
5'- A GGG CGG CAT GGC GGG CAC-3' (FRAG 765) **(SEQ. ID NO: 775)**
5'- A GGG CGG CAT GGC GGG CA-3' (FRAG 766) **(SEQ. ID NO: 776)**
5'- A GGG CGG CAT GGC GGG C-3' (FRAG 767) **(SEQ. ID NO: 777)**
5'- A GGG CGG CAT GGC GGG -3' (FRAG 768) **(SEQ. ID NO: 778)**
5'- A GGG CGG CAT GGC GG-3' (FRAG 769) **(SEQ. ID NO: 779)**
5'- A GGG CGG CAT GGC G-3' (FRAG 770) **(SEQ. ID NO: 780)**
5'- A GGG CGG CAT GGC -3' (FRAG 771) **(SEQ. ID NO: 781)**
5'- A GGG CGG CAT GG -3' (FRAG 772) **(SEQ. ID NO: 782)**
5'- A GGG CGG CAT G -3' (FRAG 773) **(SEQ. ID NO: 783)**
5'- A GGG CGG CAT -3' (FRAG 774) **(SEQ. ID NO: 784)**
5'- GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 775) **(SEQ. ID NO: 785)**
5'- GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 776) **(SEQ. ID NO: 786)**
5'- GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 777) **(SEQ. ID NO: 787)**
5'- GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 778) **(SEQ. ID NO: 788)**
5'- GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 779) **(SEQ. ID NO: 789)**
5'- GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 780) **(SEQ. ID NO: 790)**
5'- GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 781) **(SEQ. ID NO: 791)**
5'- GGG CGG CAT GGC GGG CAC AG-3' (FRAG 782) **(SEQ. ID NO: 792)**
5'- GGG CGG CAT GGC GGG CAC A-3' (FRAG 783) **(SEQ. ID NO: 793)**
5'- GGG CGG CAT GGC GGG CAC-3' (FRAG 784) **(SEQ. ID NO: 794)**
5'- GGG CGG CAT GGC GGG CA-3' (FRAG 785) **(SEQ. ID NO: 795)**
5'- GGG CGG CAT GGC GGG C-3' (FRAG 786) **(SEQ. ID NO: 796)**
5'- GGG CGG CAT GGC GGG -3' (FRAG 787) **(SEQ. ID NO: 797)**
5'- GGG CGG CAT GGC GG-3' (FRAG 788) **(SEQ. ID NO: 798)**
5'- GGG CGG CAT GGC G-3' (FRAG 789) **(SEQ. ID NO: 799)**
5'- GGG CGG CAT GGC -3' (FRAG 790) **(SEQ. ID NO: 800)**
5'- GGG CGG CAT GG -3' (FRAG 791) **(SEQ. ID NO: 801)**
5'- GGG CGG CAT G -3' (FRAG 792) **(SEQ. ID NO: 802)**
5'- GG CGG CAT GGC GGG CAC AG G CTG GGC-3' (FRAG 793) **(SEQ. ID NO: 803)**
5'- GG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 794) **(SEQ. ID NO: 804)**
5'- GG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 795) **(SEQ. ID NO: 805)**
5'- GG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 796) **(SEQ. ID NO: 806)**
5'- GG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 797) **(SEQ. ID NO: 807)**
5'- GG CGG CAT GGC GGG CAC AGG C-3' (FRAG 798) **(SEQ. ID NO: 808)**
5'- GG CGG CAT GGC GGG CAC AGG -3' (FRAG 799) **(SEQ. ID NO: 809)**
5'- GG CGG CAT GGC GGG CAC AG-3' (FRAG 800) **(SEQ. ID NO: 810)**
5'- GG CGG CAT GGC GGG CAC A-3' (FRAG 801) **(SEQ. ID NO: 811)**
5'- GG CGG CAT GGC GGG CAC-3' (FRAG 802) **(SEQ. ID NO: 812)**
5'- GG CGG CAT GGC GGG CA-3' (FRAG 803) **(SEQ. ID NO: 813)**

5'- GG CGG CAT GGC GGG C-3' (FRAG 804) **(SEQ. ID NO: 814)**
5'- GG CGG CAT GGC GGG -3' (FRAG 805) **(SEQ. ID NO: 815)**
5'- GG CGG CAT GGC GG-3' (FRAG 806) **(SEQ. ID NO: 816)**
5'- GG CGG CAT GGC G-3' (FRAG 807) **(SEQ. ID NO: 817)**
5'- GG CGG CAT GGC -3' (FRAG 808) **(SEQ. ID NO: 818)**
5'- GG CGG CAT GG -3' (FRAG 809) **(SEQ. ID NO: 819)**
5'- G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) **(SEQ. ID NO: 820)**
5'- G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) **(SEQ. ID NO: 821)**
5'- G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) **(SEQ. ID NO: 822)**
5'- G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) **(SEQ. ID NO: 823)**
5'- G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) **(SEQ. ID NO: 824)**
5'- G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) **(SEQ. ID NO: 825)**
5'- G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) **(SEQ. ID NO: 826)**
5'- G CGG CAT GGC GGG CAC AG-3' (FRAG 817) **(SEQ. ID NO: 827)**
5'- G CGG CAT GGC GGG CAC A-3' (FRAG 818) **(SEQ. ID NO: 828)**
5'- G CGG CAT GGC GGG CAC-3' (FRAG 819) **(SEQ. ID NO: 829)**
5'- G CGG CAT GGC GGG CA-3' (FRAG 820) **(SEQ. ID NO: 830)**
5'- G CGG CAT GGC GGG C-3' (FRAG 821) **(SEQ. ID NO: 831)**
5'- G CGG CAT GGC GGG -3' (FRAG 822) **(SEQ. ID NO: 832)**
5'- G CGG CAT GGC GG-3' (FRAG 823) **(SEQ. ID NO: 833)**
5'- G CGG CAT GGC G-3' (FRAG 824) **(SEQ. ID NO: 834)**
5'- G CGG CAT GGC -3' (FRAG 825) **(SEQ. ID NO: 835)**
5'- CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) **(SEQ. ID NO: 836)**
5'- CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 827) **(SEQ. ID NO: 837)**
5'- CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) **(SEQ. ID NO: 838)**
5'- CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) **(SEQ. ID NO: 839)**
5'- CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) **(SEQ. ID NO: 840)**
5'- CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) **(SEQ. ID NO: 841)**
5'- CGG CAT GGC GGG CAC AGG -3' (FRAG 832) **(SEQ. ID NO: 842)**
5'- CGG CAT GGC GGG CAC AG-3' (FRAG 833) **(SEQ. ID NO: 843)**
5'- CGG CAT GGC GGG CAC A-3' (FRAG 834) **(SEQ. ID NO: 844)**
5'- CGG CAT GGC GGG CAC-3' (FRAG 835) **(SEQ. ID NO: 845)**
5'- CGG CAT GGC GGG CA-3' (FRAG 836) **(SEQ. ID NO: 846)**
5'- CGG CAT GGC GGG C-3' (FRAG 837) **(SEQ. ID NO: 847)**
5'- CGG CAT GGC GGG -3' (FRAG 838) **(SEQ. ID NO: 848)**
5'- CGG CAT GGC GG-3' (FRAG 839) **(SEQ. ID NO: 849)**
5'- CGG CAT GGC G-3' (FRAG 840) **(SEQ. ID NO: 850)**
5'- GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) **(SEQ. ID NO: 851)**
5'- GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) **(SEQ. ID NO: 852)**
5'- GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) **(SEQ. ID NO: 853)**
5'- GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) **(SEQ. ID NO: 854)**
5'- GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) **(SEQ. ID NO: 855)**
5'- GG CAT GGC GGG CAC AGG C-3' (FRAG 846) **(SEQ. ID NO: 856)**
5'- GG CAT GGC GGG CAC AGG -3' (FRAG 847) **(SEQ. ID NO: 857)**
5'- GG CAT GGC GGG CAC AG-3' (FRAG 848) **(SEQ. ID NO: 858)**
5'- GG CAT GGC GGG CAC A-3' (FRAG 849) **(SEQ. ID NO: 859)**
5'- GG CAT GGC GGG CAC-3' (FRAG 850) **(SEQ. ID NO: 860)**
5'- GG CAT GGC GGG CA-3' (FRAG 851) **(SEQ. ID NO: 861)**
5'- GG CAT GGC GGG C-3' (FRAG 852) **(SEQ. ID NO: 862)**
5'- GG CAT GGC GGG -3' (FRAG 853) **(SEQ. ID NO: 863)**
5'- GG CAT GGC GG-3' (FRAG 854) **(SEQ. ID NO: 864)**
5'- G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) **(SEQ. ID NO: 865)**
5'- G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) **(SEQ. ID NO: 866)**
5'- G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) **(SEQ. ID NO: 867)**
5'- G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) **(SEQ. ID NO: 868)**
5'- G CAT GGC GGG CAC AGG CT-3' (FRAG 859) **(SEQ. ID NO: 869)**
5'- G CAT GGC GGG CAC AGG C-3' (FRAG 860) **(SEQ. ID NO: 870)**
5'- G CAT GGC GGG CAC AGG -3' (FRAG 861) **(SEQ. ID NO: 871)**
5'- G CAT GGC GGG CAC AG-3' (FRAG 862) **(SEQ. ID NO: 872)**
5'- G CAT GGC GGG CAC A-3' (FRAG 863) **(SEQ. ID NO: 873)**
5'- G CAT GGC GGG CAC-3' (FRAG 864) **(SEQ. ID NO: 874)**
5'- G CAT GGC GGG CA-3' (FRAG 865) **(SEQ. ID NO: 875)**

5'- G CAT GGC GGG C-3' (FRAG 866) **(SEQ. ID NO: 876)**
5'- G CAT GGC GGG -3' (FRAG 867) **(SEQ. ID NO: 877)**
5'- CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 868) **(SEQ. ID NO: 878)**
5'- CAT GGC GGG CAC AGG CTG GG-3' (FRAG 869) **(SEQ. ID NO: 879)**
5'- CAT GGC GGG CAC AGG CTG G-3' (FRAG 870) **(SEQ. ID NO: 880)**
5'- CAT GGC GGG CAC AGG CTG -3' (FRAG 871) **(SEQ. ID NO: 881)**
5'- CAT GGC GGG CAC AGG CT-3' (FRAG 872) **(SEQ. ID NO: 882)**
5'- CAT GGC GGG CAC AGG C-3' (FRAG 873) **(SEQ. ID NO: 883)**
5'- CAT GGC GGG CAC AGG -3' (FRAG 874) **(SEQ. ID NO: 884)**
5'- CAT GGC GGG CAC AG-3' (FRAG 875) **(SEQ. ID NO: 885)**
5'- CAT GGC GGG CAC A-3' (FRAG 876) **(SEQ. ID NO: 886)**
5'- CAT GGC GGG CAC-3' (FRAG 877) **(SEQ. ID NO: 887)**
5'- CAT GGC GGG CA-3' (FRAG 878) **(SEQ. ID NO: 888)**
5'- CAT GGC GGG C-3' (FRAG 879) **(SEQ. ID NO: 889)**
5'- AT GGC GGG CAC AGG CTG GGC-3' (FRAG 880) **(SEQ. ID NO: 890)**
5'- AT GGC GGG CAC AGG CTG GG-3' (FRAG 881) **(SEQ. ID NO: 891)**
5'- AT GGC GGG CAC AGG CTG G-3' (FRAG 882) **(SEQ. ID NO: 892)**
5'- AT GGC GGG CAC AGG CTG -3' (FRAG 883) **(SEQ. ID NO: 893)**
5'- AT GGC GGG CAC AGG CT-3' (FRAG 884) **(SEQ. ID NO: 894)**
5'- AT GGC GGG CAC AGG C-3' (FRAG 885) **(SEQ. ID NO: 895)**
5'- AT GGC GGG CAC AGG -3' (FRAG 886) **(SEQ. ID NO: 896)**
5'- AT GGC GGG CAC AG-3' (FRAG 887) **(SEQ. ID NO: 897)**
5'- AT GGC GGG CAC A-3' **(FRAG 888) (SEQ. ID NO: 898)**
5'- AT GGC GGG CAC-3' **(FRAG 889) (SEQ. ID NO: 899)**
5'- AT GGC GGG CA-3' **(FRAG 890) (SEQ. ID NO: 900)**
5'- T GGC GGG CAC AGG CTG GGC-3' **(FRAG 891) (SEQ. ID NO: 901)**
5'- T GGC GGG CAC AGG CTG GG-3' **(FRAG 892) (SEQ. ID NO: 902)**
5'- T GGC GGG CAC AGG CTG G-3' **(FRAG 893) (SEQ. ID NO: 903)**
5'- T GGC GGG CAC AGG CTG -3' **(FRAG 894) (SEQ. ID NO: 904)**
5'- T GGC GGG CAC AGG CT-3' **(FRAG 895) (SEQ. ID NO: 905)**
5'- T GGC GGG CAC AGG C-3' **(FRAG 896) (SEQ. ID NO: 906)**
5'- T GGC GGG CAC AGG -3' **(FRAG 897) (SEQ. ID NO: 907)**
5'- T GGC GGG CAC AG-3' **(FRAG 898) (SEQ. ID NO: 908)**
5'- T GGC GGG CAC A-3' **(FRAG 899) (SEQ. ID NO: 909)**
5'- T GGC GGG CAC-3' **(FRAG 900) (SEQ. ID NO: 910)**
5'- GGC GGG CAC AGG CTG GGC-3' **(FRAG 901) (SEQ. ID NO: 911)**
5'- GGC GGG CAC AGG CTG GG-3' **(FRAG 902) (SEQ. ID NO: 912)**
5'- GGC GGG CAC AGG CTG G-3' **(FRAG 903) (SEQ. ID NO: 913)**
5'- GGC GGG CAC AGG CTG -3' **(FRAG 904) (SEQ. ID NO: 914)**
5'- GGC GGG CAC AGG CT-3' **(FRAG 905) (SEQ. ID NO: 915)**
5'- GGC GGG CAC AGG C-3' **(FRAG 906) (SEQ. ID NO: 916)**
5'- GGC GGG CAC AGG -3' **(FRAG 907) (SEQ. ID NO: 917)**
5'- GGC GGG CAC AG-3' **(FRAG 908) (SEQ. ID NO: 918)**
5'- GGC GGG CAC A-3' **(FRAG 909) (SEQ. ID NO: 919)**
5'- GC GGG CAC AGG CTG GGC-3' **(FRAG 910) (SEQ. ID NO: 920)**
5'- GC GGG CAC AGG CTG GG-3' **(FRAG 911) (SEQ. ID NO: 921)**
5'- GC GGG CAC AGG CTG G-3' **(FRAG 912) (SEQ. ID NO: 922)**
5'- GC GGG CAC AGG CTG -3' **(FRAG 913) (SEQ. ID NO: 923)**
5'- GC GGG CAC AGG CT-3' **(FRAG 914) (SEQ. ID NO: 924)**
5'- GC GGG CAC AGG C-3' **(FRAG 915) (SEQ. ID NO: 925)**
5'- GC GGG CAC AGG -3' **(FRAG 916) (SEQ. ID NO: 926)**
5'- GC GGG CAC AG-3' **(FRAG 917) (SEQ. ID NO: 927)**
5'- C GGG CAC AGG CTG GGC-3' **(FRAG 918) (SEQ. ID NO: 928)**
5'- GGG CAC AGG CTG GG-3' **(FRAG 919) (SEQ. ID NO: 929)**
5'- C GGG CAC AGG CTG G-3' **(FRAG 920) (SEQ. ID NO: 930)**
5'- C GGG CAC AGG CTG -3' **(FRAG 921) (SEQ. ID NO: 931)**
5'- C GGG CAC AGG CT-3' **(FRAG 922) (SEQ. ID NO: 932)**
5'- C GGG CAC AGG C-3' **(FRAG 923) (SEQ. ID NO: 933)**
5'- C GGG CAC AGG -3' **(FRAG 924) (SEQ. ID NO: 934)**
5'- GGG CAC AGG CTG GGC-3' **(FRAG 925) (SEQ. ID NO: 935)**
5'- GGG CAC AGG CTG GG-3' **(FRAG 926) (SEQ. ID NO: 936)**
5'- GGG CAC AGG CTG G-3' **(FRAG 927) (SEQ. ID NO: 937)**

5'- GGG CAC AGG CTG -3' **(FRAG 928) (SEQ. ID NO: 938)**
5'- GGG CAC AGG CT-3' **(FRAG 929) (SEQ. ID NO: 939)**
5'- GGG CAC AGG C-3' **(FRAG 930) (SEQ. ID NO: 940)**
5'- GG CAC AGG CTG GGC-3' **(FRAG 931) (SEQ. ID NO: 941)**
5'- GG CAC AGG CTG GG-3' **(FRAG 932) (SEQ. ID NO: 942)**
5'- GG CAC AGG CTG G-3' **(FRAG 933) (SEQ. ID NO: 943)**
5'-GG CAC AGG CTG -3' **(FRAG 934) (SEQ. ID NO: 944)**
5'- GG CAC AGG CT-3' **(FRAG 935) (SEQ. ID NO: 945)**
5'-G CAC AGG CTG GCC-3' **(FRAG 936) (SEQ. ID NO: 946)**
5'-G CAC AGG CTG GC-3' **(FRAG 937) (SEQ. ID NO: 947)**
5'-G CAC AGG CTG G-3' **(FRAG 938) (SEQ. ID NO: 948)**
5'-G CAC AGG CTG -3' **(FRAG 939) (SEQ. ID NO: 949)**
5'-CAC AGG CTG GGC 3' **(FRAG 940) (SEQ. ID NO: 950)**
5'-CAC AGG CTG GG-3' **(FRAG 941) (SEQ. ID NO: 951)**
5'-CAC AGG CTG G-3' **(FRAG 942) (SEQ. ID NO: 952)**
5'-AC AGG CTG GGC-3' **(FRAG 943) (SEQ. ID NO: 953)**
5'-AC AGG CTG GG-3' **(FRAG 944) (SEQ. ID NO: 954)**
5'-C AGG CTG GGC-3' **(FRAG 945) (SEQ. ID NO: 955)**
5'-TTT TCC TTC CTT TGT CTC TCT TC **(FRAG 946) (SEQ. ID NO: 956)**
5'-GCT CCC GGC TGC CTG **(FRAG 947) (SEQ. ID NO: 957)**
5'-CTC GGC CGT GCG GCT CTG TCG CTC CCG GT **(FRAG 948) (SEQ. ID NO: 958)**
5'-CCG CCG CCC TCC GGG GGG TC **(FRAG 949) (SEQ. ID NO: 959)**
5'-TGC TGC CGT TGG CTG CCC **(FRAG 950) (SEQ. ID NO: 960)**
5'-CTT CTG CGG GTC GCC GG **(FRAG 951) (SEQ. ID NO: 961)**
5'-TGC TGG GCT TGT GGC **(FRAG 952) (SEQ. ID NO: 962)**
5'-GGC CTC TCT TCT GGG **(FRAG 953) (SEQ. ID NO: 963)**
5'-CCT GGT CCC TCC GT **(FRAG 954) (SEQ. ID NO: 964)**
5'-GGT GGC TCC TCT GC **(FRAG 955) (SEQ. ID NO: 965)**
5'-GCT TGG TCC TGG GGC TGC **(FRAG 956) (SEQ. ID NO: 966)**
5'-TGC TCT CCT CTC CTT **(FRAG 957) (SEQ. ID NO: 967)**

Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TTT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC CGC CTG GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC CCC GGC CTC CTG GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC CTT CTT GCT GGG CCT C TGC TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT GCC ACA GAC GAC AGG C GTB CBC CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' **(FRAG. NO. 1665) (SEQ. ID NO:1680)**
5'-CTG GGC CTC-3' **(FRAG 1666) (SEQ. ID NO: 1681)**
5'-TGC TTT TCT TTT CTG GGC CTC-3' **(FRAG 958) (SEQ. ID NO: 968)**
5'-TGT GGT CTG TTT TTT TCT G-3' **(FRAG 959) (SEQ. ID NO: 969)**
5'-GCC CTG CTG GGG CGC TCT CC-3' **(FRAG 960) (SEQ. ID NO: 970)**
5'-GCC GCC CGC CTG GCT CCC-3' **(FRAG 961) (SEQ. ID NO: 971)**
5'-GGB GCC CBT GBT GGG CBT GCC-3' **(FRAG 962) (SEQ. ID NO: 972)**
5'-GTG GTT CTT GCC CTC CTT TGG CTG-3' **(FRAG 963) (SEQ. ID NO: 973)**
5'-CCG TGC CCG CTC CCC GGC-3' **(FRAG 964) (SEQ. ID NO: 974)**
5'-CTC CTG GCG GGT GGC CGT TG-3' **(FRAG 965) (SEQ. ID NO: 975)**
5'-GGC CCG TGT TCC CCT GGG-3' **(FRAG 966) (SEQ. ID NO: 976)**
5'-GCC TGG GGC TCC CTT CTC TC-3' **(FRAG 967) (SEQ. ID NO: 977)**
5'-GCC CTT CTT GCT GGG CCT C-3' **(FRAG 968) (SEQ. ID NO: 978)**
5'-TGC TGC TGC TGG TGC TGT GGC CCC C-3' **(FRAG 969) (SEQ. ID NO: 979)**
5'-GTACACCGAGGAGCCCATGATGGGCATGCCACAGACGACAGGC-3' **(FRAG 970) (SEQ. ID NO: 980)**
5'-GTBCBCCGBGGBGCCCBTGBTGGGCBTGCCBCBGBCGBCBGGC-3' **(FRAG 971) (SEQ. ID NO: 981)**

Human Adenosine A2b Receptor Nucleic Acid & Antisense Oligonucleotide Fragments

5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG

GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT
CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC
GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG
AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT
TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC
CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG
GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC
TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA
CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT
GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCCCCCACTG CTTATAATGC
TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC
GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG
TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA
AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA
CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC
AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC
TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA
CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT
ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA
TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT TTATGGTGGA
AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG
CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA
AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG
GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC
GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG
CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG
CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG
GCGCGGTCCG GGCCCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG
TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT
GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC
ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG
CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG
CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC
ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT
GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA
CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG
GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG
TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG
GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC
TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT
GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG
GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG
AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC
CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC
CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG
TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT
ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA
ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA
ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT
CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG
CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG
GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC
AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC
CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG
CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG
TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT
TGCCTTTGGC ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA
GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA
TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA

CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGCGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGACCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG -3' **(FRAG. NO: 1670) (SEQ. ID NO:3006)**

5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC

ATTGTGAAAG ATACCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC
GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG
CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC
TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA
TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG-3' **(FRAG.NO:_)(SEQ.ID NO:2436)**

5'-CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT
CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT
GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC
GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC
TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG
CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC
CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG
GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT
GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC
TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG
GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA
GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA
CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT
TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA
TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC
TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG
GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC
ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC
CTGGAGCTAC CACCTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA
TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG
TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA
TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC
TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG
TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA
TATAGTG -3' **(FRAG. NO:_) (SEQ. ID NO:2435)**

5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG
GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA
TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG
CTCAGAAGCG GCACGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC
CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG
GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG
CCGCGGTGGG CACCGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA
CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC
GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG
CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG
AGGGGTCATT GCTCTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT
AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA
AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC
CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT
GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG
TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA
GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT
CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC
TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG
ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC
ATTGTGAAAG ATACCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC
GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG
CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC
TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA
TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG-3' **(FRAG. NO:_)(SEQ.ID NO:2425)**

5'-CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT
CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT
GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC
GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC

TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG
CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC
CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG
GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT
GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC
TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG
GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA
GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA
CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT
TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA
TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC
TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG
GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC
ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC
CTGGAGCTAC CACCTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA
TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG
TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA
TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC
TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG
TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA
TATAGTG **(FRAG. NO __) (SEQ. ID NO: 2424)**

5'-GCGCGTCCTG-3' **(FRAG. NO: 1671) (SEQ. ID NO:1686)**

5'-GCT GGG CCC CGG 3' **(FRAG. NO: 1672) (SEQ. ID NO:1687)**

5'-CGG GTC GGG GCC CCC C-3' **(FRAG. NO: 1673) (SEQ. ID NO:1688)**

5'- CGC GCC CGC G-3' **(FRAG. NO: 1674) (SEQ. ID NO:1689)**

5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3' **(FRAG 972) (SEQ. ID NO: 982)**

5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' **(FRAG 973) (SEQ. ID NO: 983)**

5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' **(FRAG 974) (SEQ. ID NO: 984)**

5'-CGG GTC GGG GCC CCC CGC GGC C-3' **(FRAG 975) (SEQ. ID NO: 985)**

5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3' **(FRAG 976) (SEQ. ID NO: 986)**

5'-CCG CGC CTC CGC CTG CCG CTT CTG-3' **(FRAG 977) (SEQ. ID NO: 987)**

5'-GCT GGG CCC CGG GCG CCC CCT-3' **(FRAG 978) (SEQ. ID NO: 988)**

5'-CCC CTC TTG CTC GGG TCC CCG TG-3' **(FRAG 979) (SEQ. ID NO: 989)**

5'-ACAGCGCGTCCTGTGTCTCCAGCAGCATGGCCGGGCCAGCTGGGCCCC-3' **(FRAG 980) (SEQ. ID NO: 990)**

5'-BCBGCGCGTCCTGTGTCTCCBGCBGCBTGGCCGGGCCBGCTGGGCCCC-3' **(FRAG 981) (SEQ. ID NO: 991)**

<u>Human Adenosine A3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT
TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG
TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT
CTG TTC CC GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA
TTCTCTCTAG TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT
TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG
GAGGGAGGGT TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT
TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC
AGATAAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT
TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA
GGACTGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG
GATTTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA
GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA
AGTGTTTGTT AGTAAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT
AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG
CTGCCTCTCT AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG
TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA
GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG
GAGGATATGC CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA
TTCTGTCGTT CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG
TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT
TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG

CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC
AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC
AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA
TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT
TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT
GAAGAGGGTT GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT
GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA
ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG
GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC
ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC
ACCTGTCCCT GTGGAGGTTC CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA
TGTTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC
GTGGTCAAGC TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC CTGGCTGACA
TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG
CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT
GTGGACCGAT ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC
AGCTGGGAAA TGACGCTACA AAGCCAGAGC CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT
AAGGTAAAAA TGATAAAGCC CTCAAGCCAC TGTGTGGGTT GGGTCCAAGT GTTCCTTGCT GCTGCCTCTC
TAACACGCCT GGTTAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG AACCAAGTGG GTCCCCAAAT
AACTATGGCG TGCAAGTGTC TGGTTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA
TTCCCAGACA GTCGCCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC
ATTTGATTCT GTTGCACACG TTCTTTTCCC TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC
CTCACATAGG TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA
GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG
GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG
CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT
TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG
CATAATCAGT GCTTCCAGCT CCGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT
CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT
TGCTGAGAGT TACTGAGCTC TGTACTTCCT CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT
TGCTTATCTT GATGGAACTC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA
ACTAAGAGCA GCAGCACTTT CAGATTCAGT CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA
TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA
GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC
TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC
TGTGGAGGTT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG CGAATTCGGG GGACATCTGT
TTGGGGAACT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG TCCTACAGCA TTCTGGAAAC
TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG
TTTCCAAGAG ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCACTGCAC
ATGGACCTCT GGGAAGACGT CTGGCGAGAG CTAGGCCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC
CTGTCCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG
TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT
GGTCAAGCTG AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT GGCTGACATT
GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT
GCCTTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG TCCTTGCTGG CCATCGCTGT
GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG
GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT GTTTGGCTGG AACATGAAAC
TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT TCCGTCATGA GGATGGACTA
CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC
ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA AGAGACAGGT GCATTTTATG
GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT
ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG
CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT
ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA
TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG
AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA
GTGCTCCCCA ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGTCCTTTCT
CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCCTTC
TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT

GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG
GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C
GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG
TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT
TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT
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CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT
TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA
GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA
ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT
AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA
GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT
AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA
ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG
ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC
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CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA
GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG
GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG
CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT
TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG
CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT
CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT
TGCTGAGAGT TCTCAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT
GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA
CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT
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ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC
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ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT
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TGAGGCTACA AAGCCAGAGC CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA
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GGTTAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG AACCAAGTGG GTCCCCAAAT AACTATGGCG
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GTTGCACACG TTCTTTTCCC TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC CTCACATAGG
TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG
TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC
TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG
TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT
CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAATCAGT
GCTTCCAGCT CCGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA
ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT
TACTGAGCTC TGTACTTCCT CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT
GATGGAACTC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA
GCAGCACTTT CAGATTCAGT CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC
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CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA
CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC TGTGGAGGTT
CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG CGAATTCGGG GGACATCTGT TTGGGGAACT
AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT
GCGGTGCATA AACCGGCTGG AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG

ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCACTGCAC ATGGACCTCT
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GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT
CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT GGTCAAGCTG
AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG
TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTTAT
GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC
TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG GCCCTGGGCC
TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT GTTTGGCTGG AACATGAAAC TGACCTCAGA
GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT TCCGTCATGA GGATGGACTA CATGGTATAC
TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA
TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA AGAGACAGGT GCATTTTATG GACGGGAGTT
CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC
AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG
CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTTGAT
CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA TTCTGAGTAG
TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG AGGGCCTGTA
TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA
ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGTCCTTTCT CTCTAATTCA
GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCCTTC TTCCCAATAG
AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA
TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT
AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C -3' **(FRAG. NO:1675) (SEQ. ID NO:3007)**

5'- CGAATTCGGG GGACATCTGT TTGGGGAACT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG
TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA
GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA
ATTTTAGACT GTCACTGCAC ATGGACCTCT GGGAAGACGT CTGGCGAGAG CTAGGCCCAC TGGCCCTACA
GACGGATCTT GCTGGCTCAC CTGTCCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC
TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC
AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT
CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT
CACAATCCAC TTCTACAGCT GCCTTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG
TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA
CTCACAGAAG AATATGGCTG GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT
GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT
TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA
TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA
AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT
GCTCTGTCAT GGCTGCCTTT ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG
TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT
AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG
GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT
TCCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA
CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC
ATTTTTCCTT TGTCCTTTCT CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT
ATTATTGTCT GTTTTCCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT
ACTGACAAAA GGCTCTAGTT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT
GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG
GGGACTTAAA CTGCTGAATT C -3' **(FRAG. NO:_) (SEQ. ID NO:2439)**

5'- CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC
TGTGTGGGTT GGGTCCAAGT GTTCCTTGCT GCTGCCTCTC TAACACGCCT GGTTAAAATA ATCCCTTTGG
ATGGTGCTGA GAACCACCTG AACCAAGTGG GTCCCCAAAT AACTATGGCG TGCAAGTGTC TGGTTCCCAG
AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA TTCCCAGACA GTCGCCTGTT CCTGCTGGGA
TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGCACACG TTCTTTTCCC
TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC CTCACATAGG TTGGACATTG GCCGGCTGCC
AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA
TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT
CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT

AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC
CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCCAC
CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC
TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TACTGAGCTC TGTACTTCCT
CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT GATGGAACTC AAAAAGCCAA
AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTTT CAGATTCAGT
CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC
CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT
GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC
CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC TGTGGAGGTT CCCCTGGGAA GGCAAGATGC
CCAACAACAG CACTGCTCTG -3' **(FRAG. NO:_) (SEQ. ID NO:2438)**

5'- GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG
TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT
TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT
TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT
TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA
AACAATTACA GTACAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG
CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT
TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA
GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA
ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT
AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA
GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT
AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA
ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG
ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC
CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCGTT
CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA
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GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG
CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT
TTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG
CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT
CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT
TGCTGAGAGT TCTCAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT
GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA
CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT
GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG
AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT
CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT
GTGGAGGTTC CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC
ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC
TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC CTGGCTGACA TTGCTGTTGG
GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCTTTTT
ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT
ACTTGCGGGT CAACCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA
TGAGGCTACA AAGCCAGAGC -3' **(FRAG. NO:_) (SEQ. ID NO:2437)**

5'-CGAATTCGGG GGACATCTGT TTGGGGAACT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG
TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA
GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA
ATTTTAGACT GTCACTGCAC ATGGACCTCT GGGAAGACGT CTGGCGAGAG CTAGGCCCAC TGGCCCTACA
GACGGATCTT GCTGGCTCAC CTGTCCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC
TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC
AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT
CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT
CACAATCCAC TTCTACAGCT GCCTTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG
TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA
CTCACAGAAG AATATGGCTG GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT
GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT

TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGTCCTTTCT CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTCCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C -3' **(FRAG. NO:_) (SEQ. ID NO:2427)**

5'-TTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA GTACAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCGTT CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG GCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTC CCTCGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC TCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC TGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC TCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC CCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AGCCAGAGC-3' **(FRAG. NO:_) (SEQ. ID NO:2426)**

5'-GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCACGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACCGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG

CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTCTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATACCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG-3'**(FRAG. NO:_)(SEQ.ID NO:2425)**

5'-GBG CB TGC-3' **(FRAG. NO:1676) (SEQ. ID NO:1691)**
5'-TTG TTG GGC-3' **(FRAG. NO:1677) (SEQ. ID NO:1692)**
5'-TGC CTT CCC BGG G-3' **(FRAG. NO:1678) (SEQ. ID NO:1693)**
5'-GTT GTT GGG CAT CTT GCC-3' **(FRAG. NO:1679) (SEQ ID NO:3)**
5'-GTG GGC CTA GCT CTC GCC-3' **(GRAG. NO:1680) (SEQ ID NO:5)**
5'-ACA GAG CA TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G-3' **(FRAG 982) (SEQ. ID NO: 992)**
5'-BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG G-3' **(FRAG 983) (SEQ. ID NO: 993)**
5'-CCC TTT TCT GGT GGG GTG-3' **(FRAG 984) (SEQ. ID NO: 994)**
5'-GTG CTG TTG TTG GGC-3' **(FRAG 985) (SEQ. ID NO: 995)**
5'-TTT CTT CTG TTC CC-3' **(FRAG 986) (SEQ. ID NO: 996)**
5'-CCC TTT TCT GGT GGG GTG-3' **(FRAG 987) (SEQ. ID NO: 997)**
5'-GTG CTG TTG TTG GGC-3' **(FRAG 988) (SEQ. ID NO: 998)**
5'-TTT CTT CTG TTC CC-3' **(FRAG 989) (SEQ. ID NO: 999)**

<u>Human IgE Receptor β Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT-3' **(FRAG. NO:1681) (SEQ. ID NO:1694)**
5'-CCC CTG GG-3' **(FRAG. NO:1682) (SEQ. ID NO:1695)**
5'-GCTCTCCTBTT-3' **(FRAG. NO:1683) (SEQ. ID NO:1696)**
5'-CBTTBBCCGBGCTG-3' **(FRAG. NO:1684) (SEQ. ID NO:1697)**
5'-TTT CCC CTG GGT CTT CC-3' **(FRAG 990) (SEQ. ID NO: 1000)**
5'-CTC CTG CTC TTT TTT C-3' **(FRAG 991) (SEQ. ID NO: 1001)**
ATTTGCTCTCCTATTACTTTCTGTGTCCATTTTTTCATTAACCGAGCTGT **(FRAG 992) (SEQ. ID NO: 1002)**
BTTTGCTCTCCTBTTBCTTTCTGTGTCCBTTTTTTCBTTBBCCGBGCTGT **(FRAG 993) (SEQ. ID NO: 1003)**

Human Fc-ε Receptor CD23 Antigen (IgE Receptor)
<u>Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TC C TTG GBT TCT CCC GB-3'**(FRAG 1685)(SEQ.ID NO:1698)**
5'-GT CCT CCT-3' **(FRAG 1686) (SEQ. ID NO: 1699)**
5'-TGT GTC TGT CCT CC-3' **(FRAG 1687) (SEQ. ID NO: 1700)**
5'-GTG GCC CTG GC-3' **(FRAG 1688) (SEQ. ID NO: 1701)**
5'-CGT GGT TGG GG-3' **(FRAG 1689) (SEQ. ID NO: 1702)**
5'-TCT CTG BBT BTT GBC C-3' **(FRAG1690) (SEQ. ID NO:1703)**
5'-GCC TGT GTC TGT CCT CCT-3' **(FRAG 994) (SEQ. ID NO: 1004)**
5'-GCT TCG TTC CTC TCG TTC-3' **(FRAG 995) (SEQ. ID NO:1005)**
5'-CTG CTT GGT GCC CTT GCC G-3' **(FRAG 996) (SEQ. ID NO: 1006)**
5'-GTC CTG CTC CTC CGG GCT GTG G-3' **(FRAG 997) (SEQ. ID NO: 1007)**
5'-GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' **(FRAG 998) (SEQ. ID NO: 1008)**
5'-CCT TCG CTG GCT GGC GGC GTG C-3' **(FRAG 999) (SEQ. ID NO: 1009)**

5'-GGG TCT TGC TCT GGG CCT GGC TGT-3' **(FRAG 1000) (SEQ. ID NO: 1010)**
5'-GGC CGT GGT TGG GGG TCT TC-3' **(FRAG 1001) (SEQ. ID NO: 1011)**
5'-GCT GCC TCC GTT TGG GTG GC **(FRAG 1002) (SEQ. ID NO: 1012)**
5'-TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA **(FRAG 1003) (SEQ.ID NO:1013)**
5'-TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB **(FRAG 1004) (SEQ.ID NO:1014)**

Human IgE Receptor α Subunit Nucleic Acid and Antisense Oligonucleotide Fragments

5'- GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GCG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' **(FRAG. NO: 1691) (SEQ. ID NO:1704)**
5'- TGG BCT CC -3' **(FRAG. NO: 1692) (SEQ. ID NO:1705)**
5'-CCB TCT GGB-3' **(FRAG. NO: 1693) (SEQ. ID NO:1706)**
5'-CT GCT BBC BCG-3' **(FRAG. NO: 1694) (SEQ. ID NO:1707)**
5'-GTT TTT GGG GTT TG-3' **(FRAG. NO: 1695) (SEQ. ID NO:1708)**
5'-GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT-3' **(FRAG. NO:1005) (SEQ. ID NO:1015)**
5'-ACAGTAGAGTAGGGGATTCCATGGCAGGAGCCATCTTCTTCATGGACTCC-3' **(FRAG.NO:1006)(SEQ.ID NO:1016)**
5'-TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC-3' **(FRAG. NO:1007) (SEQ. ID NO:1017)**
5'-BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG-3' **(FRAG. NO:1008) (SEQ. ID NO:1018)**
5'-BCT GCT BBC BCG CCB TCT GGB GC-3' **(FRAG. NO:1009) (SEQ. ID NO:1019)**
5'-GTT GTT TTT GGG GTT TGG CTT-3' **(FRAG. NO:1010) (SEQ. ID NO:1020)**
5'-GCC TTT CCT GGT TCT CTT-3' **(FRAG. NO:1011) (SEQ. ID NO:1021)**
5'-BCBGTBGBGTBGGGGBTTCCBTGGCBGGBGCCBTCTTCTTCBTGGBCTCC-3' **(FRAG.NO:1012) (SEQ.ID NO:1022)**
5'-TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' **(FRAG.NO:1013) (SEQ.ID NO:1023)**

Human IgE Receptor (Fc Epsilon R) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' **(FRAG: 1696) (SEQ. ID NO:1709)**
5'-TCG TTC CTC TCG-3' **(FRAG: 1697) (SEQ. ID NO:3001)**
5'-BGB BCG BGB C-3' **(FRAG: 1698) (SEQ. ID NO:1711)**
5'-TGB BTB TTGB-3' **(FRAG: 1699) (SEQ. ID NO:1712)**
5'-GCC TGT GTC TGT CCT CCT-3' **(FRAG. NO:1014) (SEQ. ID NO:1024)**
5'-GCT TCG TTC CTC TCG TTC-3' **(FRAG. NO:1015)(SEQ. ID NO:1025)**
5'-CTG CTT GGT GCC CTT GCC G-3' **(FRAG. NO:1016)(SEQ. ID NO:1026)**
5'-GTC CTG CTC CTC CGG GCT GTG G-3' **(FRAG. NO:1017)(SEQ. ID NO:1027)**
5'-GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' **(FRAG. NO:1018) (SEQ. ID NO:1028)**
5'-CCT TCG CTG GCT GGC GGC GTG C-3' **(FRAG. NO:1019) (SEQ. ID NO:1029)**
5'-CCC BGB BCG BGB CCC GGB CCG BCB-3' **(FRAG. NO:1020) (SEQ. ID NO:1030)**
5'-GGC CGT GGT TGG GGG TCT TC-3' **(FRAG. NO:1021) (SEQ. ID NO:1031)**
5'-GCT GCC TCC GTT TGG GTG GC-3' **(FRAG. NO:1022) (SEQ. ID NO:1032)**
5'-GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' **(FRAG. NO:1023) (SEQ. ID NO:1033)**

Human High Affinity IgE Receptor Oligonucleotide Fragments

5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA ATTAGTTATT TAATAGTTGG CACCCCAAAA CAAGTTACTT AACCTCACTA AGGTTCAGTT TTCCTGTTTA TAAAATGTAG ATACTGATAG TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT TTAGGATAAC ACCTGGCATA TGTTTGGTAT TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC ATCCCACTTT TCTAAGTTGT AAACTAAATA GTTGTACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG ATAGGGAGTG GAGTAAGTGG GTAAATATTA AATTGCCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA GAAAGAAGCA AAACCAGGCA CAGCTGATGG GTTAACCAGA TATGATACAG AAAACATTTC CTTCTGCTTT TTGGTTTTAA GCCTATATTT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG GATCTTCATG TGGAATGACT GGTTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA TGATAGAATG GTTCCTCAAG TGCTTCAGAT GTGAAGTGGG TTTAAATATA CTGTCCCTGT CTTCTTCAGA GTTTTGGTAA

AGATAAAATA GGACACTCAT TTAAAAGCAA TCTTTGCAAA TGACAAGCCA CTATAGACAT TAATAGAGTT
TTCATTTCCA GTATTATCAT TAATATCAGA TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC
AGAAGAATTA GTAAAGGAAT CCTGGAGAAA GCCCCTGCTG TGTATTTAAA GGAGAAAGGG AGATCATGTT
GGGAAATTAT AATATTAAAA GTAAACAAAA GCTAGGAAGT AAAATAAAAT AAATTATATG GCCTAGATCC
CCATAAGTAA TGGTTTAACT TCTGCCTTCC TGTGTTCTGA GCCAGATTAG GGCACAGTAG AGAAAGAGGA
GTCTCTGAAA ATGTTTCCAA TTTCGCTGGT CAGACAGCGG ATCATCAGTG AATCAGATGA AAATTTGTGG
ATTTATGCAC TAACTGATCA GCAGGAAATT AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCCAAAAG
AATTTGGCAG TTGCTAGCCA TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTTGACTT
AGGGGTTAGA TTTTATGTGT TTGAACCCCA AATTAGTTAT TTAATAGTTG GCACCCCAAA ACAAGTTACT
TAACCTCACT AAGATTCAGT TTTCCTGTTT ATAAAATGTA GATAGTGATA GTATGTACTT TATAGGATTA
TTGTGAAAAA TAAATGAAAT ATCAGATTTA TTTAGGATAA CACCTGGCAT ATGTTTGGTA TTCAGTAATT
AGTTGCTGCT GTTTTATTCT GCTCTCCCTT GCATCCCACT TTTCTAAGTT GTAAACTAAA TAGTTGTACA
CAGATTGACA GATTAAGAAA GGCTTGTGAT TGTGCTAGAC CTATGCCTCT CTCTCACCAG ATTCCAGGTG
TATATGTGGA GGTGGGATAG GGAGTGGAGT AAGTGGGTAA ATATTAAATT GCCCAGTTGG GCACCATCCT
GAATATTATC TCTAAAGAAA GAAGCAAAAC CAGGCACAGC TGATGGGTTA ACCAGATATG ATACAGAAAA
CATTTCCTTC TGCTTTTTGG TTTTAAGCCT ATATTTGAAG CCTTAGATCT CTCCAGCACA GTAAGCACCA
GGAGTCCATG AAGAAGATGG CTCCTGCCAT GGAATCCCCT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC
GGTAAGTAGA GATTCAATTA CCCCTCCCAG GGAGGCCCAA ATGAATTTGG GGAGCAGCTG GGGTAGGAAC
CTTTACTGTG GGTGGTGACT TTTTCTAGGA CATGTGCAAA CTATTGGGCA TTTCCCAGGG ACTCTGTAGT
GGAGCCAAGC TAGAAAGCAG AGGCAAGTGG GCTGAGCAAC ACCTAAGGAG GAAGCCAGAC TGAAAGCTTG
GTTCCTTGCA TTTGCTCTGG CATCTTCCAG AGTGCAAATT TCCTACCAAG GTAATGAGGG TAGAGGAGAG
AAAGAAGCTC TTTCTTCCCC TGATTCTCAT TCCTGAAAAG ACGGTTGGTC CTTAAAATTC CATGGATGTA
GATCTTATCC CCACACCCAG ATTCTAGTCC TCTGGAGATA AAGAAGACTG CTGGACACTA ATGTATCCTC
TCTGGACTTT TGCAGCTCCA GATGGCGTGT TAGCAGGTGA GTCCTCTGTT CTTGTTCCCT TGGTGTATCA
ACATGTCTGG GCATTGCTTT CCTCTCACTA TTTTCTTCGT CCCATCACTT CTGCTTTCTA ATGAGCATGA
ATCTGTTCCT TGGCCAGACT ACTTTCCCTC TCCACCTTGC CTTGTCTTTC TTTTTTTCCC TGATTCATTG
CATTCTCTCA AGTCATTCTC TCCTCTGTTT TAGTCAATAA CCATGTCTGT TGCACATATA CATGTCTCAT
TCTCTCTCCT AGACACTTTG GCATGATCTC GCTCAATAAT TACATTATTA TTATTATTGC CATTTTATAA
TTGAGGATGC TGAAACTCAG TGATTTTCTG GTGGTTACAT GGCTAAGGAA CTGGATTTCA ACGTAAGTTC
CTTGGATCTA AGTCCAGTTC TCTTCTGACT ATATCACCCT TTTGTTATCA CCATGTATCT ACTTCTTTGG
TCTCTGTTCA AATTTGCACT ACATCCCCTT GTTCCAGGAA GCCATTCAAG ACTGACTTTC TTAGTGCCTC
TCACTACTTT CTGGAACTGA CATATGTTTT TCACTCTGTA TATACTTACA ATTAAATAGT CATAAATATT
CAGAGCTTGG AGAAACCTTA TATTTCATCC AGTCCAGTAA ATTTATCCAT CCATAATTCA CTCATTCATT
CACATAATAA ATATTTAATG TAACAATGGT TGAACATGGC AGACAGTGTT TCTACCTCAA AAGAGATTGC
AGTCCTCATT TACAGATACT GAATTGAAAT TAACAGAAGT AGAGTGAGTC AGCTCAAATC ACATAGTGAA
TTGGTTTCTT TGTTTTTAAA TCTCCTGCAT ATGTGTCCTG TCTTTCTCCC TGTGTTGGGC GTTCCCTGGG
GCACCAATAC TAATTTCTCC TTCCCCTAGA AATCAAAACA GGGTCTTATC ACCAACAGAA TAAGGACAGG
TTGACCACTG ATTCTCAGAA TATTGCTTCG TTTGTACTTT TAAGCCTAGA CAGTTTTCAA TGACTTTTTT
TCTCTCTACA TGTCTTTTCA TATTTTTATC TTCTTGAAGT CCCTCAGAAA CCTAAGGTCT CCTTGAACCC
TCCATGGAAT AGAATATTTA AAGGAGAGAA TGTGACTCTT ACATGTAATG GGAACAATTT CTTTGAAGTC
AGTTCCACCA AATGGTTCCA CAATGGCAGC CTTTCAGAAG AGACAAATTC AAGTTTGAAT ATTGTGAATG
CCAAATTTGA AGACAGTGGA GAATACAAAT GTCAGCACCA ACAAGTTAAT GAGAGTGAAC CTGTGTACCT
GGAAGTCTTC AGTGGTAAGT TCCAGGGATA TGGAAATACA GATCTCTCAT GTGAGGGATG GCTCATCTGA
AGATGGGAAA AAACAGGTTA TTCCAAGGGT TAGGACACCA GAGTGGGATT CAAGGCCTCT CATTTTTAAG
ACCCCTGCAT TGGCTGGGCA CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCAGGTGG
ATCACGAGGT CAGGAGATCG AGACCATCCG GCTAACATGG TGAAACCCCA TCTCTGCTAA AAAATATATA
TATATAAAAT TAGCCGGGCG TAGTGGTGGG CACCTGTAGT CCCAGGTACT CGGGAGGCTG AGGCAGGAGA
ATGGTGTGAA CCCAGGAGGT GGAGGTTGCA GTGAGCTGAG ATCACGCCAC TGCCCTCCAG CCTGGGCTAC
AGAGCAAGAC TCCGTCTCAA AAAATAAATA AATAAATAAA AAAGACCCCT GCATCTCTTT TCTTCTACCC
CCTTCCCTTT TGATTACTTG TATGCCTTCT TTCAATATTC TAGTCATCTC TCAATATTAT TCCTCCACCC
TATTTTCCTC TATCTTTTCT GCCTAGATTC AGGTATATAT TATGTGGTCA AACAGCATGA CATATATGTG
AACATTTCAA AGACCTGTGT ATCTGGAATA GGATCAAAAG GTTTGACTTA AAGTTTTGCT CTGCATAATC
CATATGGCAG GACCTGAATA TTAGGTTGTA CTCTTCGTTA TGAAACATAT CTGGGTACAT TTCCTTATGT
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AGTCACAGTC ACACACACAT ATGTATTACT TACACTATAT ATAACTTCCT ATGCAAATAT TTTACCACCA GTCAATAATA CATTTTTGCC AAGACATGAA GTTTTATAAA GATCTGTATA ATTGCCTGAA TCACCAGCAC ATTCACTGAC ATGATATTAT TTGCAGATTG ACAAGTAGGA AGTGGGGAAC TTTTATTAAG TTACTCGTTG TCTGGGGAGG TAAATAGGTT AAAAACAGGG AAATTATAAG TGCAGAGATT AACATTTCAC AAATGTTTAG TGAAACATTT GTGAAAAAAG AAGACTAAAT TAAGACCTGA GCTGAAATAA AGTGACGTGG AAATGGAAAT AATGGTTATA TCTAAAACAT GTAGAAAAAG AGTAACTGGT AGATTTTGTT AACAAATTAA AGAATAAAGT TAGACAAGCA ACTCGTTGAC TAATACATTA AGCGTTTGAG TCTAAGATGA AAGGAGAACA CTGGTTATGT TGATAGAATG ATAAAAAGGG TCGGGCGCGG AGGCTCACGC CTGTAATCCC AGCCCTTTGG GAGGCCGAGG TGGGCAGATC ACGAAGTCAG TAGTTTGAGA CCAGCCTGGC CAACATAGTG AAACCCCGTC TCTACTAAAA ATACAAAAAA AAAATTAGCT GGGTGTGGTG GCAGTCACCT GTAGTCCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCAGTGCAC TCCAGCCTTG GTGACAATGG GAGACTCCAT CTCAAAAAAA AAAAAAAAAA AAAAAAGATA AAAAGTCAGA AATCTGAAAA GTGGAGGAAG AGTACAAATA GACCTAAATT AAGTCTCATT TTTTGGCTTT GATTTTGGGG AGACAAAGGG AAATGCAGCC ATACAGGGCC TGATGACATC CAATACATGA GTTCTGGTAA AGATAAAATT TGATACACGG TTTGGTGTCA TTATAAGAGA AATCATTATT AAATGAAGCA AGTTAACACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA CTAAGGATAA AATCTAGCCT AGAAGATACA ATAATTAGTC ATAAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA AAATAGAGAA AGATTAGATA AAGAGAAAAT AAGTATCCAT CAGAGACAGT ATCTCTAGGC TTGGGCAAGA GAAAAGTCCA CAGTGATAAG CAACTCCACC TAAGGCATGA ATATGCGGCA GAGAAAACAG CAATAGTGAA TGAATGCAAA AGGTGCTGAG CAAATTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTGC AAAGACCTTT AGAGAAAGAG AATGGGAGCA TATGTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA AAAAATTCTG TTTATAAAAG AAGGAAAAGA TAGTTTATGT TTTTAGCCTA AGTATAAGAG TCCTACAGAT GGACTGAAAA AAATCAGTCT GAGAGTATTA GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT AGATTGTGAA AGTGATCACG ACAATCACAC AACAAATAAT TAAGTGACTT GGTATGCTTT ATTTAATTGT AGGGCCTGAG GTTTTCCATT CTCATTTTTC TAAAATACAA TTTTGTTTCT CCAAATTTGA CAGCAGAATA AAAACCCTAC CCTTTCACTG TGTATCATGC TAACCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTCACA TACAGACTCT TAACCCTGGT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTTA CAGTTGTATA GTATATGATA TCTCTTTTAT TTCACTCAAT TTATATTTTC ATCATTGACT ACATATTTCT TATACACAAC ACACAATTTA TGAATTTTTT CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG CCCACCTCAG GCAGACACAG AGCACAATGC TGGGGTTCTC TTCACACTAT CACTGCCCCA AATTGTCTTT CTAAATTTCA ACTTCAATGT CATCTTCTCC ATGAAGACCA CTGAATGAAC ACCTTTTCAT CCAGCCTTAA TTTCTTGCTC CATAACTACT CTATCCCACG ATGCAGTATT GTATCATTAA TTATTAGTGT GCTTGTGACC TCCTTATGTA TTCTCAATTA CCTGTATTTG TGCAATAAAT TGGAATAATG TAACTTGATT TCTTATCTGT GTTTGTGTTG GCATGCAAGA TTTAGGTACT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAAATGATG CCAAAGACCA AGAGCAGTTT CTGAAGTCCT CCTTTTCATC AGCTCTTTAT CAAACAGAAC ACTCTATAAA CAACCCATAG CCAGAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG AGCATGAGTC ATATTTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTTT TTCTCTTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA AATTTGGAAC AAAAGATTCC TAACTGGTCT TTCTGTTCCC ATATTCTGTG ATTTTTCAAT ATTTAGGATT TTTGGTAATC ACAATTACTT AGTTTGTGGT TGAGATAGCA ACACGAATCA GAACTATTTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA AAGAAGTGAT GCNGGTCGTG GTGGCTCACG CCTGTAATCC CAGCACTTTA GGGAGGCCAA GGCGGGTGGA TCACGAGGTC AGGAGATCGA GACCATCCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA AAATTAGCCA GGCGTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCCTGGG CAAAAGAGCA AGACTGCGTC TCAAAAAAAA AAAAAAAAAA AAAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA TAATATTTTT CTAAATCCCT CTGAAAAATG CTAATCAAAG GGTTTTTTTC CTAAAAATTG TCTTAGAAAT AAAATTTCCC CTTTGGGAGA CCGAGGCTGG CAGATCACGA GGTCAGGAGA TAGAGACCAC GGTGAAACCC CGTCTCTACT AAAAATACTA AAAATTAGCC GGGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG GAGGCTGAGG CTGGAGAATC ACGTGAAC-3' **(FRAG. NO:_)(SEQ. ID NO:2505)**

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GCCTATATTT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG-3' **(FRAG. NO:_)(SEQ. ID NO:2500)**

5'-GATCTTCATG TGGAATGACT GGTTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA
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GCTAATAATA ATAACCAAAA CCTTCGGCTC TGAAAACAGT CCAGGACTGA ATAAGATCTT GGGCAAAAGA
ACTAGACAGT TTTGGTTTAT TTTCCCTTTC ATTTTATGTC TTCATCATAG TCATTGGAGG CTCATTCTTC
TTGTCATGGA GTAAATGGGA TTAAAGTTC-3' **(FRAG. NO:_)(SEQ. ID NO:2501)**

5'-TACTAAGAGT CTCCAGCATC CTCCACCTGT CTACCACCGA GCATGGGCCT ATATTTGAAG CCTTAGATCT
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TCAAGTACTG GTATGAGAAC CACAACATCT CCATTACAAA TGCCACAGTT GAAGACAGTG GAACCTACTA
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GCTCAATTAA CATTGGTTGA ATAAATGAGA GAATGAATAG ATTCATTTAT TAGCATTTGT AAAAGAGATG
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AAAAAAAA-3′ (FRAG. NO:_)(SEQ. ID NO:2502)

5’-TCTCAATATA ATAATATTCT TTATTCCTGG ACAGCTCGGT TAATGAAAAA ATGGACACAG AAAGTAATAG
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5’-AAGCTTTTCA AAGGTGCAAT TGGATAACTT CTGCCATGAG AAATGGCTGA ATTGGGACAC AAGTGGGGAC
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CATTTCCTCA TAAAGACTTT AAATTGCTAG GACGAGAATG GCCAACAGGA GTGAAGGATT CATAACTTTA
TCTTTACTTA GATGTAAAGA ACAATTACTG ATGTTCAACA TGACTACATA CATAAAGGCG CATGGAGAAA
AGTATTGGCC TTCCATGCAT TAGGTAGTGC TTGTATCAAT TCTTATAGTG GCTAGGGTAT CCTGGAAAAT
CTTACGTGTG GATCATTTCT CAGGACAGTC TAGGACACTA ACGCAGTTTC TCATGTTTGG CTTCTATTAT
TAAAAAATGA TACAATCTCG GGAAAATTTT TTTGATTTTC ATGAAATTCA TGTGTTTTTC TATAGGTAAC
ACAAATTCTG ACTGCTATGA TATGCCTTTG TTTTGGAACA GTTGTCTGCT CTGTACTTGA TATTTCACAC
ATTGAGGGAG ACATTTTTTC ATCATTTAAA GCAGGTTATC CATTCTGGGG AGCCATATTT GTGAGTATAT
ATCTATAATT GTTTCTGAAA TAACACTGAA CATAGGTTTT TCTCTTTCTC AGATCTAACC AGTTGTTTAT
TCCCAGTATT AAGATGATAT TTATAATTCT TAATTATAAA TATATGTGAG CATATATAAC ATAGATATGC
TCATTAACAA CAACAAAAGA TTCTTTTTAC AATTAACGGT GGGTTAAACA TTTAGCCCAC AGTTTTATCC
CATGAGAAAC CTGAATCTAA TACAAGTTAA ATGACTTGCC TAAGGGCCAC TTGACTAATA GTAATTGAAC
CTAAACTTTC AGAATCCAAC TCCAGGAACA TACTTCTAGC ACTATTCATC AATAAAGTTA TATGATAAAT
ACATACAACT TTATCTGTCA ACTAAAAATA ACAACAGAGG CTGGGCATGG TGGCTCACAC CCGTAATCCC
AGCACTTTGG GAGCCTGAGG CAGGTGGATC ACCTGAGGTC AGGAGTTTGA GACCAGCCTG ACCAACATGG
TGAAACCTCA TCTCTACTAA ATATAAAAAA TTAGCTGAGT GTGATAGTGC ATACCTGTAA TCCAGCTACT

TAAGAGGCTG AGGCAGGAGG CTTGTTTGAA CCTGGAAGGC AGAGGTTGCA GTGAGCTGAG ATTGTGCCAT
TGCACTCCAG CCTGGGCAAT AAGTGCGAAC TCTGTCTCAA AATAATAATA ATAATAATAG AAAATAAAGT
TGTCTTCATG AAAAATGAGG AAAGAGATTG CTGGGGTGAG AAACATTAAG ATCAATGGGC ATATGGTGAC
CTTCTATGCC CTAGAAACTC TTTTANGGTA TTTTCTCCTG GTATCTCTTT TACNCATCGT TCTATCTGGA
AAAATAGGTG GATGAGTGAG ATAATAACGG TATATACTTT TTAAAGGTCT AATTGACATA TATAAATTGC
AAGTATTTCA GATGTCAATT TGCTAACCTT GACACACATA GACACACATG AAAACATCAC CACATTAATA
CAATGTATGT ATCCATCATT CCAAAAGCTT CCCTGTGTAT CTTTGTAACT CTTTCTTCCT CCCTCCACTC
CTTGTCCTCT CGTTCCCAAG AAAACATTGA TCTGCTTCCT GTGAATATAA ATTAACTTAC ATTTTTTAGA
GCTTTATATA AGTATGTTCT CTTTACTGTT TGTCTTCCTT CGCTGCACAG TTATTTTGAG ATTCTTCAAG
TTTTTTCTTT ATATCGATAC TTCATTCACA AGAATATATT TTAATTCTAG ACTATGTCAC ATTGACTTTG
TCGTCTGCTA AATCCTTAGT GCTCAGATGA CTTGTTCAGG ACTCTCCTTG AACCTGTACC TCTGTTANAT
TGAAACTTGT CTCTACTGTC TTTTTATTTC AAACACAGCT TATTAGGTGT CTCTCAACCC ATCAAACNCA
CAATCTGAGT CTTTAGGAGA TTGCTTTGAA TTTGTGCTAT TGACTTATAT NTATATNAAA TNTGTAAATG
TTTGGTAAAA ATATCATCAT GTACNTTTTC ATAATTACGC TATNTNCACA TGATATATGT CAGACTCTGG
AAATATGCAT GCCACAGACA CGTGTTTCTT GCCTAAAGGG GCTGATGGAA GACNCACATA CNAATAGACG
ATTGCAGTAG AATGAGAGTG GTGGTCTAAN CAGTACATGT CCTGATGTTG CTCGGACAGT TACTACNCCA
AGAGTACCCC CTGCATTGTC AGGGTTAGCA TCTCCTGGAA GCCTCATGTA AATGAAGAAT TTCATGCTCC
ATCCAGGACC TAATGAATAA GAATCTGCAT TTTAGCAAGA CCCTCATATG ATTCATATAC ACTTTTTTTT
TTTTTTTTTA GATGGAGTCT CACTCTTGTC GCCCAGGCTG GAGTGCAATG GCATGATCTT GGCTCACTGC
AACCTCTGCC TCCCGGGTTC AAGTGATTCT CCTGTCTCAG CCTCCCTAGT AGCTGGGACT ACAGGTGCAT
GCCACAGTGG CTGGCTAATT TTTGTATTTT TAGTAGAGAC AGGGTTTCAC CATTTTGGTC AGGCTGGTCT
TGAACTCATG ACCTCCGGTG ATTCCCCCGC CTCGGCTTCC CAAAGTGCTG GGATTACAGA CATGAGCCAC
CACACCCGCC TTATTCGTAT ACNCATTTAA TTCTGAGAAG CACTCTATAG AAAATAAGAA TAAGAAAATA
TTGGGCTCAC AGGTGACATT AATAAGTAAC TTTATCGAGT ACCCCAAATT TTACCTATGT TTGGAAGATG
GGGTTAAAAG GACACATTGA AAACAAGAAC TCATTGTGGC TTTTTTTTCC TCCTTTTTGA ACAGTTTTCT
ATTTCTGGAA TGTTGTCAAT TATATCTGAA AGGAGAAATG CAACATATCT GGTGAGTTGC CCGTTTCTGT
CTTTGTCCAT CCTTGAAAAG ATAAGAAGAA CAGAGTTTTA AGAGTCTTAA GGGAAACACA TCTTTGTCTC
CTATATTACT TGTCAATGTG GATATATGAT TTTGTTTCAA TCTATTTTGT GTCCTAAGGC TTTTTGCAAC
AGAAGTTGGA TATATCATTA GAAACATAAA TTGTACCATT TAACATACAT GAAGTTTATG TTTACCTTGA
CGTTCTTCTA AAAAGTGTCC TACACCGGCA TTGTCCTTGT AGGCATATTC ACATGATCAA ATAAAATAAT
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TGAGAAAGTA ATATATGCTT CATTAAACAA TGCGGACATT TTCAGGGTTT CCCTTTTTAA CCAAAATTTG
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GTGCAGGCCC AGGTCTGAGT GTTCTTCATT ATTATCAGGT GAGAGGAAGC CTGGGAGCAA ACACTGCCAG
CAGCATAGCT GGGGGAACGG GAATTACCAT CCTGATCATC AACCTGAAGA AGAGCTTGGC CTATATCCAC
ATCCACAGTT GCCAGAAATT TTTTGAGACC AAGTGCTTTA TGGCTTCCTT TTCCACTGTA TGTATTTTTT
TTTGTGTGGG AAGACTAAGA TTCTGGGTCC TAATGTAAGT AAGAAGCCCT CTTCTCCTGT TCCATGAACA
CCATCCTTTT CTGTAACTTC TATTACACAG TATAGTGGTT CTGTAAGTTC ACACAGCCCA GGGAGATGCT
GGCTGCCCAC TCCCCTCAAC CCAGGCAAAT TCCTCGGGGT TAAAGTTATC TACTGCAAGT GACGATCTCT
GGGTTTTTCT GTGCCTGTGT TTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTATGTGTCA CTTTAAAAGG
ACTGGTCAGA TGGTAGGGAG ATGAAAACAG GAGATGCTAT AAGAAAATAA ACTTTTGGGG CGAATACCAA
TGTGACTCTT TTTGTTTGTC ATTTGTTGCT GTTCAATAGG AAATTGTAGT GATGATGCTG TTTCTCACCA
TTCTGGGACT TGGTAGTGCT GTGTCACTCA CAATCTGTGG AGCTGGGGAA GAACTCAAAG GAAACAAGGT
AGATAGAAGC CCGATATAAA ATCTTGAATG ACAGGTTAAC GAATTGGAGC TTTATTCCTT AAAATATGGC
CTGGGTTTTC TGAAACATTT CTTCCAGAAA ATAGTTTCTC CAAGTTTTAT TACTTTGGTT TACAAATCTC
ACATTTAAAT CACATTTTAT ACCATAAGTA GCACACATTT CATAATATTC CTCTGAATGA GGGTTGGGAT
AATAGGACTG ATATGTTAGA AATGCCTTAA AGTGTGTGGA GCATGAGAGA TGGATGTACA GAAGGCTTGT
GAGGAAACCA CCCAGGTATC TGGCCTTGTT TTCTGCCCCA GAACTAGCCG CCTATTCCTG TTTCTGTTTT
ATTCCTTTGT TTCTTGACTT TTCCTTTCCA ACTTGCTCTA AAACCTCAGT TTTCTTTCCT TTCTGATTCA
TGACTACCAA ATGTTTTCAC TTGCCTCACC CGTCCATTAC ACCTTTGATA AGAACCACCA GACCTTGTGC
TCATGTACTT GCCCATGTCT GATGGAAGAA ACATACTCTC TCCATCTGTC CACTTTCCTG AGGCATTCAA
GTCTAGCCAC CTTTTAAAAT CACTCTCCTC CAGGCTGGGC ACGGTGTCAC GCCTGTAATC TCAGCACTTT
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AACAAAAACA GAAAAGGAAA CATTAGCCCA GCGTGGTGGC AGGTACCTGA GGTTCCAGAT ACTTGGGAGG
CTGAAGCAGG AGAATCGCTT GAGCCCAAGA GATGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACCA
CAGCCAGGGT GACAGAGCCA TACTTCCCAG CACATTGGGA GGCCAAAGCT GAAGAATAAT TTGAGGTGAG
GATTTGGAGA CCAGCCTGGC CAACATGGTG AAACTCCGTC TGTACTAAAA ATATAAAACT TAGTGGGGCA
TGGGGGCACA CACCTGTAAT TTCAGCTACT TAGGAGGCTG AGGCAGGAGA ATTGCTTGAA CCCGGGAGGC
GGAAGTTGCA GTGAGCCAAG ATCGTGGCCA CTGCACTCCA GCCTGGGTGA CATAGTGAGA TTCTGTCTCA
AAAAAAATAA AAGAAATTTA AAAAATCACT CTCTTCCAAA GATAGATAAA TAAGACAGCA GATATACTAA
GGAATAACCT CACCAACTTG TCATTGACTG ACATGATTTC TTTTGGCCCA CTTGGCCAGC TAGTCTGGTT

TGGTTTTCTG GAAATGAAAG AAATAATCAG AGTTTAATGA CAGAGAGCGT GAGACCCAGA AAGACAAAAG
TAGATGAGGT AAGTCTCTTG AGCGAGACTT CTAGGGATGG GAAATTTGTG GTGATTGATA TGAAATGATT
TTTCCCTTAT CAGCTTCCAG AGGATCGTGT TTATGAAGAA TTAAACATAT ATTCAGCTAC TTACAGTGAG
TTGGAAGACC CAGGGGAAAT GTCTCCTCCC ATTGATTTAT AAGAATCACG TGTCCAGAAC ACTCTGATTC
ACAGCCAAGG ATCCAGAAGG CCAAGGTTTT GTTAAGGGGC TACTGGAAAA ATTTCTATTC TCTCCACAGC
CTGCTGGTTT TACATTAGAT TTATTCGCCT GATAAGAATA TTTTGTTTCT GCTGCTTCTG TCCACCTTAA
TATGCTCCTT CTATTTGTAG ATATGATAGA CTCCTATTTT TCTTGTTTTA TATTATGACC ACACACATCT
CTGCTGGAAA GTCAACATGT AGTAAGCAAG ATTTAACTGT TTGATTATAA CTGTGCAAAT ACAGAAAAAA
AGAAGGCTGG CTGAAAGTTG AGTTAAACTT TGACAGTTTG ATAATATTTG GTTCTTAGGG TTTTTTTTTT
TTTTAGCATT CTTAATAGTT ACAGTTGGGC ATGATTTGTA CCATCCACCC ATACCCACAC AGTCACAGTC
ACACACACAT ATGTATTACT TACACTATAT ATAACTTCCT ATGCAAATAT TTTACCACCA GTCAATAATA
CATTTTTGCC AAGACATGAA GTTTTATAAA GATCTGTATA ATTGCCTGAA TCACCAGCAC ATTCACTGAC
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TAAATAGGTT AAAAACAGGG AAATTATAAG TGCAGAGATT AACATTTCAC AAATGTTTAG TGAAACATTT
GTGAAAAAAG AAGACTAAAT TAAGACCTGA GCTGAAATAA AGTGACGTGG AAATGGAAAT AATGGTTATA
TCTAAAACAT GTAGAAAAAG AGTAACTGGT AGATTTTGTT AACAAATTAA AGAATAAAGT TAGACAAGCA
ACTGGTTGAC TAATACATTA AGCGTTTGAG TCTAAGATGA AAGGAGAACA CTGGTTATGT TGATAGAATG
ATAAAAAGGG TCGGGCGCGG AGGCTCACGC CTGTAATCCC AGCCCTTTGG GAGGCCGAGG TGGGCAGATC
ACGAAGTCAG TAGTTTGAGA CCAGCCTGGC CAACATAGTG AAACCCCGTC TCTACTAAAA ATACAAAAAA
AAAATTAGCT GGGTGTGGTG GCAGTCACCT GTAGTCCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC
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ATAGAGGGCC TGATGACATC CAATACATGA GTTCTGGTAA AGATAAAATT TGATACACGG TTTGGTGTCA
TTATAAGAGA AATCATTATT AAATGAAGCA AGTTAACACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA
GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA CTAAGGATAA AATCTAGCCT AGAAGATACA
ATAATTAGTC ATAAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA AAATAGAGAA AGATTAGATA
AAGAGAAAAT AAGTATCCAT CAGAGACAGT ATCTCTAGGC TTGGGCAAGA GAAAAGTCCA CAGTGATAAG
CAACTCCACC TAACGCATGA ATATGCGGCA GAGAAAACAG CAATAGTGAA TGAATGCAAA AGGTGCTGAG
CAAATTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTGC AAAGACCTTT AGAGAAAGAG
AATGGGAGCA TATGTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA
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GGACTGAAAA AAATCAGTCT GAGAGTATTA GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA
TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT AGATTGTGAA AGTGATCACG ACAATCACAC
AACAAATAAT TAAGTGACTT GGTATGCTTT ATTTAATTGT AGGGCCTGAG GTTTTCCATT CTCATTTTTC
TAAAATACAA TTTTGTTTCT CCAAATTTGA CAGCAGAATA AAAACCCTAC CCTTTCACTG TGTATCATGC
TAAGCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTCACA
TACAGACTCT TAACCCTGGT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTTA CAGTTGTATA
GTATATGATA TCTCTTTTAT TTCACTCAAT TTATATTTTC ATCATTGACT ACATATTTCT TATACACAAC
ACACAATTTA TGAATTTTTT CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG
CCCACCTCAG GCAGACACAG AGCACAATGC TGGGGTTCTC TTCACACTAT CACTGCCCCA AATTGTCTTT
CTAAATTTCA ACTTCAATGT CATCTTCTCC ATGAAGACCA CTGAATGAAC ACCTTTTCAT CCAGCCTTAA
TTTCTTGCTC CATAACTACT CTATCCCACG ATGCAGTATT GTATCATTAA TTATTAGTGT GCTTGTGACC
TCCTTATGTA TTCTCAATTA CCTGTATTTG TGCAATAAAT TGGAATAATG TAACTTGATT TCTTATCTGT
GTTTGTGTTG GCATGCAAGA TTTAGGTACT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAAATGATG
CCAAAGACCA AGAGCAGTTT CTGAAGTCCT CCTTTTCATC AGCTCTTTAT CAAACAGAAC ACTCTATAAA
CAACCCATAG CCACAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA
AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG
AGCATGAGTC ATATTTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTTT
TTCTCTTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA AATTTGGAAC AAAAGATTCC TAACTGGTCT
TTCTGTTCCC ATATTCTGTG ATTTTTCAAT ATTTAGGATT TTTGGTAATC ACAATTACTT AGTTTGTGGT
TGAGATAGCA ACACGAATCA GAACTATTTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA
AAGAAGTGAT GCNGGTCGTG GTGGCTCACG CCTGTAATCC CAGCACTTTA GGGAGGCCAA GGCGGGTGGA
TCACGAGGTC AGGAGATCGA GACCATCCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA
AAATTAGCCA GGCGTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA
TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCCTGGG CAAAAGAGCA
AGACTGCGTC TCAAAAAAAA AAAAAAAAAA AAAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA
TAATATTTTT CTAAATCCCT CTGAAAAATG CTAATCAAAG GGTTTTTTTC CTAAAAATTG TCTTAGAAAT
AAAATTTCCC CTTTGGGAGA CCGAGGCTGG CAGATCACGA GGTCAGGAGA TAGAGACCAC GGTGAAACCC
CGTCTCTACT AAAAATACTA AAAATTAGCC GGGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG
GAGGCTGAGG CTGGAGAATC ACGTGAAC-3' (FRAG. NO:_)(SEQ. ID NO:2504)

Human Histidine Decarboxylase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CTC TGT CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC-3'**(FRAG. NO:1700) (SEQ. ID NO:1711)**

5'-GGC TCT GGC **(FRAG. NO:1701) (SEQ. ID NO: 1712)**

5'-CCC TTG G **(FRAG. NO:1702) (SEQ. ID NO: 1713)**

5'- TT TGT TCT TCC **(FRAG. NO:1703) (SEQ. ID NO: 1714)**

5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' **(FRAG. NO:1024) (SEQ. ID NO: 1034)**

5'- TCT CTC TCC CTC TCT CTC TGT -3' **(FRAG. NO:1025) (SEQ. ID NO:1035)**

5'- CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC-3' **(FRAG. NO:1026) (SEQ. ID NO:1036)**

5'- TTT TGT TCT TCC TTG CTG CC-3' **(FRAG. NO:1027) (SEQ. ID NO:1037)**

5'- GCC CCG CTG CTT GTC T TC CTC G-3' **(FRAG. NO:1028) (SEQ. ID NO:1038)**

5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC **(FRAG.NO:1029)(SEQ.ID NO:1039)**

Human Beta Tryptase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' **(FRAG. NO:1704) (SEQ. ID NO: 1715)**

5'- GCT CCT GGG GGC CT-3' **(FRAG. NO:1705) (SEQ. ID NO: 1716)**

5'-CGT BGG CGC-3' **(FRAG. NO:1706) (SEQ. ID NO: 1717)**

5'-T GGC CTG GGG-3' **(FRAG. NO:1707) (SEQ. ID NO: 1718)**

5'-CTT GCT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1030) (SEQ. ID NO:1040)**

5'-GTC CCT CCG GGT GTT CCC GGC-3' **(FRAG. NO:1031) (SEQ. ID NO:1041)**

5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TCG-3' **(FRAG. NO:1032) (SEQ. ID NO:1042)**

Human Tryptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3' **(FRAG. NO: 1708) (SEQ. ID NO:1719)**

5'-CT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1709) (SEQ. ID NO:1720)**

5'-B TCC TGG CCB CGG BBT TCC -3' **(FRAG. NO:1710) (SEQ. ID NO:1721)**

5'-GTC CCT C-3' **(FRAG. NO:1711) (SEQ. ID NO:1722)**

5'-CTT GCT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1033) (SEQ. ID NO:1043)**

5'-GTC CCT CTG GCT G TT CCC GGC-3' **(FRAG. NO:1034) (SEQ. ID NO:1044)**

5'-CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC -3' **(FRAG. NO:1035) (SEQ. ID NO:1045)**

Human Prostaglandin D Synthase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGT GTG CGG GGC CTG GTG CC CCT GGG CCT CGG GTG CTG CCT GT GCG CTG CCT TCT TCT CCT GG GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT GCC CTG GGG GTC TGG GTT CGG CTG T CCC CBG CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG-3'**(FRAG.NO:1712)(SEQ.ID NO:1723)**

5'-T TCT CCT GCB GCC GBG -3' **(FRAG. NO:1713) (SEQ. ID NO:1724)**

5'-CTT GCT GCC CTG GCT GT-3' **(FRAG. NO:1714) (SEQ. ID NO:1725)**

5'- TCT TCT CCT GG-3' **(FRAG. NO:1715) (SEQ. ID NO:1726)**

5'-GGT GTG CGG GGC CTG GTG CC-3' **(FRAG. NO:1036) (SEQ. ID NO:1046)**

5'-CCT GGG CCT CGG GTG CTG CCT GT-3' **(FRAG. NO:1037) (SEQ. ID NO:1047)**

5'-GCG CTG CCT TCT TCT CCT GG-3' **(FRAG. NO:1038) (SEQ. ID NO:1048)**

5'-GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT-3' **(FRAG. NO:1039) (SEQ. ID NO:1049)**

5'-GCC CTG GGG GTC TGG GTT CGG CTG T-3' **(FRAG. NO:1040) (SEQ. ID NO:1050)**

5'-CCC CBG CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG -3' **(FRAG. NO:1041) (SEQ. ID NO:1051)**

Human Cyclooxygenase-2 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGG CGC GGG CGB GCB TCG C TTT GGG CTT TTC TCC TTT GGT T TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG-3' **(FRAG. NO: 1716) (SEQ. ID NO:1729)**

5'-G GCB GGG -3' **(FRAG. NO: 1717) (SEQ. ID NO: 1730)**

5'-TCC TTT GGT T-3' **(FRAG. NO:1718) (SEQ. ID NO:1731)**

5'- GGG CGC GGG CGB GCB TCG C-3' **(FRAG. NO:1042) (SEQ. ID NO:1052)**

5'- TTT GGG CTT TTC TCC TTT GGT T-3' **(FRAG. NO:1043) (SEQ. ID NO:1053)**

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' **(FRAG. NO:1044) (SEQ. ID NO:1054)**

Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC-3' **(FRAG. NO: 1719) (SEQ. ID NO: 1732)**

5'-TTC TCC TTT GGT T-3' **(FRAG. NO:1720) (SEQ. ID NO: 1733)**

5'-T TTC TCC TTT GGT T-3' **(FRAG. NO:1721) (SEQ. ID NO:1734)**

5'- GGG CGC GGG CGB GCB TCG C-3' **(FRAG. NO:1042) (SEQ. ID NO:1052)**

5'- TTT GGG CTT TTC TCC TTT GGT T-3' **(FRAG. NO:1043) (SEQ. ID NO:1053)**

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' **(FRAG. NO:1044) (SEQ. ID NO:1054)**

Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' **(FRAG. NO: 1722) (SEQ. ID NO: 1735)**

5'-TTC CTG T-3' **(FRAG. NO:1723) (SEQ. ID NO: 1736)**

5'-CTC TTT CTG CT-3' **(FRAG. NO: 1724) (SEQ. ID NO:1737)**

5'-CCC CTT CTG TCC C-3' **(FRAG. NO:1725) (SEQ. ID NO: 1738)**

5'- GCC CTG CTG CTC TTT CTG CT-3' **(FRAG. NO:1047) (SEQ. ID NO:1055)**

5'- TCC CTT GGT GGG TTG GGC C-3' **(FRAG. NO:1048) (SEQ. ID NO:1056)**

5'- GCT GGT TGT TCT GGG GTT C-3' **(FRAG. NO:1049) (SEQ. ID NO:1058)**

5'- TTG CTG CCC CTT CTG TCC C-3' **(FRAG. NO:1050) (SEQ. ID NO:1057)**

5'- TGT TTG CTG GTG TCT GCG C -3' **(FRAG. NO:1051) (SEQ. ID NO:1059)**

5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' **(FRAG. NO:1052) (SEQ. ID NO:1060)**

Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCCT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC AGAGATGCAT CTGCTCCCAG CCCTGGCAGG GGTCCTGGCC ACACTCGTCC TCGCCCAGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CCTGGGGCAG TGGAGACCTC GGTCCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGCGTTGACT GTGAGAGGAC CTGCGCCCAG CTGCCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT GGCCTCCCCC AAACGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGCCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA CCCTCTTTAT GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA

TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT
TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG
GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC
AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT
AGCTTCCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCCATCCT
CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC
CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC
ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT
TCTGGGAAGA CCCTGGTACC CGACTGCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG
ACAGCGCAAG GCCCTGAGCA GAATTTCCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT
TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA
ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG
GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC
TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC
CCTAGGACTT TGGGGGGAAA TTAGGAGCAT CCAACTA GAATTCCGTG GCCAGGACCC CTGCCAGGGC
ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC TGCGAGACTG CATAGCAGAG GCCAAGTTGC
TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC
CATGGACCTC CTGTCCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC CGCAGATTAT
ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG
ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA
GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCCTT GCTAGGGGCC
TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA
CCCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT
CCCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTCATGC AGTGGGGCCA GTTCATTGAC
CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC TGTGAGAGGA
CCTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCCGCATCA AGAACCAGCG
TGACTGCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC
AACGCGCTCA CCTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC
GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT
GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCCTG
GCAGGTGACA CCCGATCAAC GGAAACCCCC AAACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA
ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG GAATGGAGAC AAACTGTACA ATGAGGCTCG
GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC
CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT
TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG
GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA
GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT
TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA
CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCCAG
CCCCGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC AGGACTTGGC AAGGAAGTTC CTGAATTTGT
ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTTGCCGG GGGCTCGAGT
GGGGCCTCTT CTGCCTTGTC TGTTCGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC
AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTC CTTGTCTCGA ATTATATGTG
ACAATACCGG TATCACCACG GTTTCAAGGG ACATCTTCAG AGCCAACATC TACCCTCGGG GCTTTGTGAA
CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC
CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT
GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG GGTTCCCCAG CCAGGAGTGA AGGCTGGGGG
CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC
AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCCAGG CAAGAAAAGT CAGCTGGAGG GTTTACAGCA
CTTTCTACTG TTTCCCAGCC CTCCCTCCCC TCCCTCACCA TGACTAAGAG ACCACTCGGT CCTAGCCTCC
AGACACCCCA CAACACTCCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC
CGGAATTC-3' **(FRAG. NO: 1726) (SEQ. ID NO: 3008)**
5'-CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG
GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC
CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG
AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA
GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG
AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC
AGAGATGCAT CTGCTCCCAG CCCTGGCAGG GGTCCTGGCC ACACTCGTCC TCGCCCAGCC CTGTGAGGGC
ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAGGGGA AGCACTTGGG
TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CCTGGGGCAG
TGGAGACCTC GGTCCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC

CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT-3' **(FRAG. NO:_)(SEQ. ID NO:2483)**

5'-TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGCGTTGACT GTGAGAGGAC CTGCGCCCAG CTGCCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT GGCCTCCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG-3' **(FRAG.NO:_)(SEQ.ID NO:2484)**

5'-CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGGCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC-3' **(FRAG.NO:_)(SEQ.ID NO:2485)**

5'-TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA CCCTCTTTAT GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC-3' **(FRAG.NO:_)(SEQ.IDNO:2486)**

5'-CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG GGTGAGGGTG GGAGCATGC CCTCCCCTAG GTGG-3' **(FRAG.NO:_)(SEQ.ID NO:2487)**

5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT AGCTTCCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTCCCACCA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT TCTGGGAAGA CCCTGGTACC-3' **(FRAG.NO:_)(SEQ.ID NO:2488)**

5'-CGACTGCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA GAATTTCCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGGAAA TTAGGAGCAT CCAACTA-3' **(FRAG.NO:_)(SEQ.ID NO:2489)**

5'-GAATTCCGTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGTCCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGGACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTCATGC AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCCGCATCA AGAACCAGCG TGACTGCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC AACGCGCTCA CCTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC AAACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG GAATGGAGAC AAACTGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT

CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC
CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC
TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC
CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG
GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT
GCTTGGAGGC GCTTCTGTGG GCTCTCCCAG CCCCGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC
AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT
CGCTGAGCCT CTTTTGCCGG GGGCTCGAGT GGGGCCTCTT CTGGCTTGTC TGTTCGAGAA CCAGTTCAGA
AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGCCCTGA
GCAGAATTTC CTTCTCTCGA ATTATATGTG ACAATACCGG TATCACCACG GTTTCAAGGG ACATCTTCAG
AGCCAACATC TACCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA
GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC
ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG
GGTTCCCCAG CCAGGAGTGA AGGCTGGGGG CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA
GGTATTAGGC TATCAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCCAGG
CAAGAAAAGT CAGCTGGAGG GTTTACAGCA CTTTCTACTG TTTCCCAGCC CTCCCTCCCC TCCCTCACCA
TGACTAAGAG ACCACTCGGT CCTAGCCTCC AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG
CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC-3' (FRAG.NO:_) (SEQ.ID no:2490)
5'-TC GGC CTG GTC CCG G-3' **(FRAG. NO: 1727) (SEQ. ID NO:1740)**
5'-TGG GGG TTT CCC TTG-3' **(FRAG. NO: 1728) (SEQ. ID NO: 1741)**
5'-TG GTC CCG GBG BGC -3' **(FRAG. NO: 1729) (SEQ. ID NO: 1742)**
5'-GCG CTC GGC CTG GTC CCG G-3' **(FRAG. NO:1053) (SEQ. ID NO:1061)**
5'-GGG TCT CCT CTT GTT GTT GC-3' **(FRAG. NO:1054) (SEQ. ID NO:1062)**
5'- TTG CGC CTC CTG CTG GGG GT CC-3' **(FRAG. NO:1055) (SEQ. ID NO:1063)**
5'-CTC TGT TCT TGT TTT GGG GGC-3' **(FRAG. NO:1056) (SEQ. ID NO:1064)**
5'-GGG CCC GGC CGT TGT CTT G-3' **(FRAG. NO:1057) (SEQ. ID NO:1065)**
5'-GTT TGG GGG TTT CCG TTG-3' **(FRAG. NO:1058) (SEQ. ID NO:1066)**
5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' **(FRAG. NO:1059)(SEQ. ID NO:1067)**
5'-GGC CGT GGT CCC GGC TTC GTT GC-3' **(FRAG. NO:1060) (SEQ. ID NO:1068)**
5'-CCT GTC TCC GTC TCG GCT CTT CTG-3' **(FRAG. NO:1061) (SEQ. ID NO:1069)**
5'-GGG CCT TGC GCT GTC TTT GGT G-3' **(FRAG. NO:1062) (SEQ. ID NO:1070)**
5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC -3' **(FRAG. NO:1063) (SEQ. ID NO:1071)**

Human Intercellular Adhesion Molecule-1 (ICAM-1)
<u>Nucleic Acid and</u> <u>Antisense Oligonucleotide Fragments</u>

5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3' **(FRAG. NO: 1730) (SEQ. ID NO: 1743)**
5'-GGG GGC TGC TGG G-3' **(FRAG. NO: 1731) (SEQ. ID NO:1744)**
5'-T GTC CTC CGG CCT CCC-3' **(FRAG. NO:1732) (SEQ. ID NO:1745)**
5'-G CCB TBG CGB GCC TGB G-3' **(FRAG. NO: 1733) (SEQ. ID NO: 1746)**
5'-CTC TGG GGT GGC CTT C-3' **(FRAG. NO:1734) (SEQ. ID NO:1747)**
5'-GCG CGG GCC GGG GGC TGC TGG G-3' **(FRAG. NO:1064) (SEQ. ID NO:1072)**
5'-GGT TGG CCC GGG GTG CCC C-3' **(FRAG. NO:1065) (SEQ. ID NO:1073)**
5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' **(FRAG. NO:1066) (SEQ. ID NO:1074)**
5'-GTG TCT CCT GGC TCT GGT TCC CC-3' **(FRAG. NO:1067) (SEQ. ID NO:1075)**
5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' **(FRAG. NO:1068) (SEQ. ID NO:1076)**
5'-GCT CCC GGG TCT GGT TCT TGT GT-3' **(FRAG. NO:1069) (SEQ. ID NO:1077)**
5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' **(FRAG. NO:1070) (SEQ. ID NO:1078)**
5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' **(FRAG. NO:1071) (SEQ. ID NO:1079)**
5'-TGC CCT GTC CTC CGG CGT CCC-3' **(FRAG. NO:1072) (SEQ. ID NO:1080)**
5'- CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3' **(FRAG. NO:1073) (SEQ. ID NO:1081)**

Human Vascular Cell Adhesion Molecule 1 (VCAM-1)
<u>Nucleic Acid and</u> <u>Oligonucleotide Fragments</u>

5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC

CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GCC BTT TTB BGT TGC TGT CGT-3'**(FRAG.NO:1735)(SEQ.ID NO:**<u>1748)</u>
5'-C TGT CGT-3' **(FRAG. NO:1736) (SEQ. ID NO:**<u>1749)</u>
5'-TGC TTC TTC C-3' **(FRAG. NO:1737) (SEQ. ID NO:**<u>1750)</u>
HSVCAM1AS1: 5'-CCT CTT TTC TGT TTT TCC C-3' **(FRAG. NO:1074) (SEQ. ID NO:**<u>1082)</u>
HSVCAM1AS2: 5'-CTC TGC CTT TGT TTG GGT TCG-3' **(FRAG. NO:1075) (SEQ. ID NO:**<u>1083)</u>
HSVCAM1AS3: 5'-CTT CCT TTC TGC TTC TTC C-3' **(FRAG. NO:1076) (SEQ. ID NO:**<u>1084)</u>
HSVCAM1AS4: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' **(FRAG. NO:1077) (SEQ. ID NO:**<u>1085)</u>
HSVCAM1AS5: 5'-GTC TTT GTT GTT TTC TCT TCC TTG-3' **(FRAG. NO:1078) (SEQ. ID NO:**<u>1086)</u>
CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT**(FRAG. NO:1079)(SEQ. ID NO:**<u>1087)</u>

Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)
<u>Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC TTC TGT C CGT TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT
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CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT
TATTGTCAGC AAACGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAACTCCA
TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG
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(SEQ. ID NO: 3009)

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ATTTCATGCC AATACTTGGA AGTTTATAAT TAAGTAAGTT TGTTTGTTAT TTTTTACTTT TTAGAAAATG
TTTTCCATAT TCCCCAATCT TAATTATTCA TGATTCTTTA GATTGCATTT AAAACATTTT GTGTGAATTT
AATGTTCACT GACACTGCTG TCTGATAATC CAGATATTCT ACATGTAGCT CTCAAGCCAA ATTGGACTTC
TTTACCCTGT GGCCTCTAAA ATTAAAAAAA ATGTTCTTCC TAGTTAGCTA GTACTTCAGA AATAATGGGC
CATGGGCCAG ACTAGAACTT AACCACTTTT CTTCTGCTAC TGTTGTTTAA CCAGCTATCA AGTATCCTAT
TTCTAGGATT AGATAAATTG ATAACTATAA TTAAAACTGA ATATAATCTT TTCATTAGGT ACTTTTAAGT
TGTTCACACT TAATTCCATT TGTACAGTAA TTTTAACTTT CTGAAACTGA AGCATTTTAA AGGGTCACCA
GGGATAGTGC CTGTAGCATT CATCAGATTC TTAGGGGTGA GAGGAGATGT GGTTGAGATG TAAAAATGGT
TAAGAATATC TACTTTATAC ACATACATAA AACATTAAAG GTCAGTGTAT TTTCAGGTCT TAGGTACTTT
TCTTGTACTA CCAGGACATT AAGTTGCCAT TCAGTGGTTA AGAGTGTTGC CTGGGAGCTG TATCACATGT
GCTTAAATCC ATTCTTGAAA TCATTTACTC CTTCTGAGCC CTTGGGCTAT TTGGTTAATT TCTCTGAACG
TTAGTTTGCT CATCTGAAAA TGGAAATAAT AATAGCAACT TCTTGACAGG GTTATAGTGA GAATTGAGTT
CATCACTGTG AAATGCTTAG AAATGTGCAT GACACATAGT TAATACTCAA GGAATTAGCC ACATCACTAT
CATCATCACT GATTATCTTC CACTCTTACC CTCTTCCAGT TCATTTTCTG CCCAGCAGAA TGATCTTTTA
AAAAGTAAAT CAGATCATGT TACTCTATTG CTTGAAGTCT ATCCCATTTG ATTAAGAATA ACAACCTAAT
CCTCTGTGGA TGCTGCCTCC TTCACCAGCC TGTCTCATGC TGCTCTCCCT ACTCTTAGTT CCTCAAACAT
ACCAAACTCT CCTGTCCCAG AGTCTTTTCG TGGTTTTTCC ATCTGCCTAG GATGCTTCTC TCTCCTATTT

TGTGTACCTT GCTAACTCCT GCTTACTGTC TTTCAGTTCT CAGCTTAAGA GTTATATCTT CATGATAACA
TTCTTTGATA TCCTTACCCT AAGATTAAGT TAGATTGATA TCCTTACCCT AAGAATAAGT TAGATTAGGT
CTCTCTATTG TAGCACCTTA GACTCTGTCA TTTGACAAAT CACAGCCCTA ATTAATTATT CTTAAAATTA
TTTAACATTC TCTCTCATGC TAGACCACAA GTTTCATGCA GGTAAGGCGG AGATTGTGTC CATTTGTTTG
ACCCCTTTGT CTCCAGGGCC TGGTAGAATG CCTCATACAT AGTAAGAATT CAATTAATAT TTTACACAGA
GAAAAAATTA GCAACTTATT TAAACAAATA TAACTGCTTC AGAGGTAAAC TGGGCACATC TTAGTTATAT
TATGTGATAT ATGATGCTTT TTGATTGTTT TTTTAAATGT TCTACAAGGT AGATATTGTT AGAGGTCCTA
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TCCTTCCATT CTTGTTTACA GTTAGCTGAG CAGATGACAC AGTCAGATGC ACAGGTAAAA TTTGGGCTAA
TAGCATTTTA AACAGCAACT CTTATTTTCT TTGGCAGTTA GTAAATCTCA TTTGAATGTC TGGGTCAGTC
TATTTAAGAG GATTTTAATT TATTTCATTT GGGTGTTTTT TTTTGATCTG TGGGATTATT TATATCCCAT
AATTACTTTT CACCCAGAGC ATTGTATTAG ATTCCTAACT GCTGTCATTG CCTCTGGGGT CTGCCTGGCT
CCCTCTTTGC TTGGTAACTG GTTGGTCACA GCATTCTTCT CAGAATCCTT TCATTCTTTT CTGCATGAGA
ACAAAAATTC TTTTGTTCAT ATTTGTATAA GATCTGATAT AGCTGCAATC AATCTTGCAT TTTTTCTTCA
CCAACGCATT GCGACCTTTA GGGATACAAG TATGTTTGTG CATGTATATG TATGTATCAG TCTTTTAAAT
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CCAAGCTGGA GTGCAGTGGT ATGACCTTGG CTCACTGCAG CCTCTGCCTC ACGGGTTCAA GGGATCGTTC
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CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACCGCGCCCA GCCTATATGT AATAATTTTA ATGGGACCAT
GAATTGAATA TTTCTTCCTT GAATAGCAAT GACATAGCCC CTTCTATTGT ACATCTGCAA GCTGATACAG
GGAATTCCTT TGTACCTGCG CTCTTCCCTG CCAGTCAGCT ATGGGGGTGA AAGTGTAGGG GTTCATCCAA
GTCCTAAAAC TGGTAGCAAC TCCTAGGGCA GGGCTGATCT GGAAGGACAG ACCCTAGGGG AGGGTGGAAC
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AACCTCCTCC TTTTTCAGTT TCCTTCTTGC TTCTCTTGAC ACCACAGAGT TTGCAGCTAG TACTTGGAGA
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TTTGGGACTG ATAAATGTGA CCAGTTCTGC TTACTGTCCA TTGCCTGAAA TGGAGCTTTG AGGTGGACTG
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CTATAACAAA ATCCCTTAAA CTGGGTAAGG GATTATAAAT ATTAGAAATT TATCTCTCAC AGTTCTGGAA
GCTGGGAAGC CCAATATCAA GGCACCAGTA GATTTGGTGT CTAACGAGGG TGTGCCGTCT GCTTCAAAAA
TGGCCCCTTG TTGCTGCATC CTCACTTAGT GCAAGGGGCA AGACAGCTCC CTTCAACCTC TTTTATAAGG
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CAATTAAGTC TTGAAATTGG TTTCAAAAAG AGAATATTCT ATTAGAGTTT TTAATGTATA GTTTTAACAT
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TCTGTCGCCC AGGCCGGACT GCGGACTGCA GTGGCGCAAT CTCGGCTCAC TGCAAGCTCC GCTTCCCGGG
TTCACGCCAT TCCCCTGCCT CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCTGCCACCG CGCCCGGCTA
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CAATTATTTA GTTTTTCTAT AAACAGGGAA ATTTATTTGT GTGGCCCTTA GAACTAATTT AATTTCCACT
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GAGTTTGAGA CCACACTGAG CAACACAGGG AGACCCCCAT CTCTACAAAA AATAAAAAAA TTCTCCAGGC
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CACACCTTCT TTGTTGGCAT TAAGATGCAA ACTTTGTTTT AAACAGTTGA GTAAATCAAA GATGGGACTG
TTAAGTTATT TGTGTTATTT ACCTGCTTTT TGAAAATGTA AAAATAAAAC TCTAGGTTTA ATTAGTAGTA
TGCTATTTAG TAATGAAGTA AAGCTAGAGG CTTCGAACAA ATCTTGTGTA ATTTCCTCTT GAATGAGAGA
GAAAATTTAA AGTAAGCAAA CAAATAAGTT GTGTGTCACC ACTCATTCAG TCATTTAACA AGTATTTCCA
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TAATCGAAAA GGCTGAGTGT GGTGACCCAT GGCTGTAATC CCAGCACTTT GGGAGGCCGA GGTGGGCAGA
TTGCTTGAGC TAGGAGTTCG AGACCAGGCT GGCCAACATG GTGAAACCCC GTCTCTACTA AAAATACAAA
AATTAGCCAG GAGTGATGGT GCGCACCTGT AATGCCAGCT ACTTGGGAGG CTGAGGCAGG AGGATCACTT
GAACCCAGGA GGTGGAGGTT GAAGTAAGCC GAGGTCATGC CACTGCACTC CAGCCTGGGC AACAGAGTGA
GACTCCATCT CAAAAAAAAA AAAAATGATC AAAGAAAGGT GAATTTTCAT CTACCCTATT TCTGCTGAGG
AAAATGGACT ATTTTCAAAT ATTTTTAATA AGGGTCAAAA TGAGGGATC-3' **(FRAG.NO:_)(SEQ.ID NO:2480)**

5'-CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CCAAAACGGA
AAGTATTTCA AGCCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTTCTCTCA
GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA
CTTATGATGA GGCCAGTGCT TATTGTCAGC AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA
GATTGAGTAC CTAAACTCCA TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC
AATGTGTGGG TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC
CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG
GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC
AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA CTTGCAAGTG TGACCCTGGC TTCAGTGGAC
TCAAGTGTGA GCAAATTGTG AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA
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TCACCATGTA AAACAGTCAT CTGGTAGATT TTTAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT
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AAGCAGATTT AACAATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC
AGTAATTGCC AAACCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT CCATTAACTT

AGCATGTGTT GAAAAAAAAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT TTAAAGGGGC AGAAAAACTC TGGGAAATAA GAGAGAACAA CTACTGTGAT CAGGCTATGT ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT TGTAAATATT TATGTAAACT GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAAT TTTAAATTAT AACTTAAAAT ATTTTATAAT TTTTAAAGTA TATATTTATT TAAGCTTATG TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT-3' **(FRAG.NO:_)(SEQ.ID NO:2479)**

5'-CCT TGC CTG CTG G-3' **(FRAG. NO: 1739) (SEQ. ID NO: 1752)**
5'-GTT GTC CC-3' **(FRAG. NO: 1740) (SEQ. ID NO:1753)**
5'-GTT CTT GGC TTC TTC TGT C-3' **(FRAG. NO:1080) (SEQ. ID NO:1088)**
5'-GGC TGG TGG-3' **(FRAG. NO:1083) (SEQ. ID NO:1092)**
5'-CGT TGG CTT CTC GTT GTC CC-3' **(FRAG. NO:1081) (SEQ. ID NO:1089)**
5'-TGT GGG CTT CTC GTT GTC CC-3' **(FRAG. NO:1082) (SEQ. ID NO:1090)**
5'-CCC TTC GGG GGC TGG TGG-3' **(FRAG. NO:1083) (SEQ. ID NO:1091)**
5'-GGC CGT CCT TGC CTG CTG G-3' **(FRAG. NO:1084) (SEQ. ID NO:1093)**

Human P Selectin Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO: 1741) (SEQ. ID NO: 1754)**
5'-TCC TTT CTT TTC-3' **(FRAG. NO: 1742) (SEQ. ID NO: 1755)]**
5'-CTC CTT TT-3' **(FRAG. NO:1743) (SEQ. ID NO:1756)**
5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' **(FRAG.NO:1085)(SEQ. ID NO:1094)**
5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO:1086) (SEQ. ID NO:1095)**

Human Endothelial Monocyte Activating Factor Nucleic Acid & Antisense Oligonucleotide Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO: 1744) (SEQ. ID NO: 1757)**
5' -CC TTT CTT TTC **(FRAG. NO: 1745) (SEQ. ID NO: 1758)**
5'-CTG TTC CTC CTT TT-3' **(FRAG. NO:1746) (SEQ. ID NO:1759)**
5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' **(FRAG.NO:1087)(SEQ. ID NO:1096)**
5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO:1088) (SEQ. ID NO:1097)**

Human IL3* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC **(FRAG. NO: 1747) (SEQ. ID NO: 1760)]**
5'-G GBG GCB CTC-3' **(FRAG. NO: 1748) (SEQ. ID NO: 1761)**
5'-GT GGG GCT CTG-3 **(FRAG. NO:1749) (SEQ. ID NO:1762)**
HUMIL3AAS1: 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' **(FRAG.NO:1089)(SEQ.ID NO:1098)**
HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CCG TGG CC-3' **(FRAG. NO:1090) (SEQ. ID NO:1099)**
GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC **(FRAG. NO:1091) (SEQ. ID NO:1100)**

Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG GGC TGC GTG CGC GTT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA GAC AGG GCA CGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC-3' **(FRAG. NO: 1750) (SEQ. ID NO: 1763)**
GBG GTG CC-3' **(FRAG. NO: 1751) (SEQ. ID NO: 1764)**
5'- GCC CCG C-3' **(FRAG. NO:1752) (SEQ. ID NO:1765)**
5'-TCTGGGGTGTCCTG **(FRAG. NO:1092) (SEQ. ID NO:1101)**
5'-GCCTTCGTGGTTCC **(FRAG. NO:1093) (SEQ. ID NO:1102)**
5'-TCTTCCTTCGTTTGC **(FRAG. NO:1094) (SEQ. ID NO:1103)**
5'-CGTCCGCGGGGGCCCCCGGGCCT **(FRAG. NO:1095) (SEQ. ID NO:1105)**
5'-GGC TGC GCT CCT GCC CCG C **(FRAG. NO:1096) (SEQ. ID NO:1104)**

5'-CTCTTTCCCGGGCTCTT **(FRAG. NO:1097) (SEQ. ID NO:1106)**
5'-GCGCTGGGGGGTGCTCC **(FRAG. NO:1098) (SEQ. ID NO:1107)**
5'-CGTGTGTTTGCGCCCTCCTCCTGGTCGC **(FRAG. NO:1099) (SEQ. ID NO:1108)**
5'-GCTTGTCGTTTTGC **(FRAG. NO:1100) (SEQ. ID NO:1109)**
5'-GGCCGGCTTTGCCCGCCTCCC **(FRAG. NO:1101) (SEQ. ID NO:1110)**
5'-GGCGCCTGGCCCGGCC **(FRAG. NO:1102) (SEQ. ID NO:1111)**
5'-TTCCTGGGCTGCGTGCGC **(FRAG. NO:1103) (SEQ. ID NO:1112)**
5'-GTTCTGTTCTTCTTCCTGGC **(FRAG. NO:1104) (SEQ. ID NO:1113)**
5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC CGG BBC GCB GGB 5' CBG BGG TGC C **(FRAG. NO:1105) (SEQ. ID NO:1114)**

Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT GBG BCC CBT TBB TBG GTG TCG B-3' **(FRAG. NO: 1753) (SEQ. ID NO: 1766)**
5'-GCC GGC BCB-3' **(FRAG. NO: 1754) (SEQ. ID NO: 1767)**
5'-T TCC TTC-3' **(FRAG. NO:1755) (SEQ. ID NO:1768)**
5'-CTC TGG TTG GCT TCC TTC-3' **(FRAG. NO:1106) (SEQ. ID NO:1115)**
5'-GCCGGCBCBTGCTBGCBGGBBGBBCBGBGGGGGBBGCBGTTGGGBGGTGBGBCCCBTTBBTBGGTGTCGB-3' **(FRAG. NO:1107) (SEQ. ID NO:1116)**

Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G -3'**(FRAG. NO: 1756)(SEQ ID NO:1769)**
5'-TCTGCGC-3' **(FRAG. NO: 1757) (SEQ ID NO: 1770)**
5'-CCT GCT CCT GGG G **(FRAG. NO:1758) (SEQ. ID NO:1771)**
5'-TCTGCGCGCCCCTCCTCC **(FRAG. NO:1108) (SEQ. ID NO:1117)**
5'-CGCCCGGCTTCTCT **(FRAG. NO:1109) (SEQ. ID NO:1118)**
5'-CGTGTGGGCTTCGG **(FRAG. NO:1110) (SEQ. ID NO:1119)**
5'-CCCCGCGCCTCCGTTGTTCTC **(FRAG. NO:1111) (SEQ. ID NO:1120)**
5'-TGCTCGCTGGGCTTG **(FRAG. NO:1112) (SEQ. ID NO:1121)**
5'-GGTTTCCTGGGGCCCTGGGTTTC **(FRAG. NO:1113) (SEQ. ID NO:1122)**
5'-TCTGCCGGGTCGTTTTC **(FRAG. NO:1114) (SEQ. ID NO:1123)**
5'-GGGTGCTGGCTGCG **(FRAG. NO:1115) (SEQ. ID NO:1124)**
5'-CTTGGTGCTGGGGCTCC **(FRAG. NO:1116) (SEQ. ID NO:1125)**
5'-GGCGGCTGCGGGCTGGGTTGGG **(FRAG. NO:1117) (SEQ. ID NO:1126)**
5'-CTTGGCTGGTTCCTGGCCTCGGG **(FRAG. NO:1118) (SEQ. ID NO:1127)**
5'-CCTCCTCCTCCTCCTCGCTCCCTTTTTCTTCCTCT **(FRAG. NO:1119) (SEQ. ID NO:1128)**
5'-TCCCTGCTGCTCTC **(FRAG. NO:1120) (SEQ. ID NO:1129)**
5'-TGCCCTCCCTTCCCTCCTGG **(FRAG. NO:1121) (SEQ. ID NO:1130)**
5'-GGTGCCTCCTTGGCCCCTGC **(FRAG. NO:1122) (SEQ. ID NO:1131)**
5'-GGCTGCTCCTTGCCCC **(FRAG. NO:1123) (SEQ. ID NO:1132)**
5'-CTCTGGGTCGGGCTGGC **(FRAG. NO:1124) (SEQ. ID NO:1133)**
5'-GGGGCGTCTCTGTGC **(FRAG. NO:1125) (SEQ. ID NO:1134)**
5'-CTGGCCTGGGTGCC **(FRAG. NO:1126) (SEQ. ID NO:1135)**
5'-GCCTCTCCTGGGGGGGTGGCTCCCTGTCC **(FRAG. NO:1127) (SEQ. ID NO:1136)**
5'-CCTTTTCCCCCGGCTCC **(FRAG. NO:1128) (SEQ. ID NO:1137)**
5'-GTGGGGGCTTTGGC **(FRAG. NO:1129) (SEQ. ID NO:1138)**
5'-GGG GGT CTG TGG CCT GCT CCT GGG G **(FRAG. NO:1130) (SEQ. ID NO:1139)**
5'-AGGGGTCTGGGGCCCTC **(FRAG. NO:1131) (SEQ. ID NO:1140)**
5'-TTTTGGGGGTCTGCCTTG **(FRAG. NO:1132) (SEQ. ID NO:1141)**
5'-GCCTGGCTGCCTTCC **(FRAG. NO:1133) (SEQ. ID NO:1142)**
5'-GGGGCCTGCCGTGGGGC **(FRAG. NO:1134) (SEQ. ID NO:1143)**
5'-TGTCCTCTGTTGCTCCCCTT **(FRAG. NO:1135) (SEQ. ID NO:1144)**
5'-TGCCTGCTGTCTGG **(FRAG. NO:1136) (SEQ. ID NO:1145)**
5'-GGTTCCCGCCTTCCCT **(FRAG. NO:1137) (SEQ. ID NO:1146)**

5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GAC CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG CCA CCC CAT TGG GAG ATG CCA AGG CAC CAG GCT G **(FRAG. NO:1138) (SEQ. ID NO:1147)**
5'-GTT CCC BGB GCT TGC CBC CTG CBG CBG GBC CBG GCB GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG CCB CCC CBT TGG GBG BTG CCB BGG CBC CBG GCT G-3' **(FRAG. NO:1139) (SEQ. ID NO:1148)**

<u>Human IL5* Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-TCCCTGTTTC CCCCCTTTCG TTCTGCGTTT GCCTTTGGCG TTTTTTGTTT GTTTCTCTC TCCGTCTTTC TTCTCCCCT GTGGGBBTTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB TGCBGBBGCB TCCTCBTGGC TCTGBBBCGG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC AAGAGCTAGC AAACTCAAAT GCAGAAGCATC CTCATGGCTC TGAAACG-3' **(FRAG. NO: 1759) (SEQ. ID NO: 1772)**
5'-GCC CCG GG-3' **(FRAG. NO: 1760) (SEQ. ID NO: 1773)**
5'-G GGT TTC T-3' **(FRAG. NO: 1761) (SEQ. ID NO: 1774)**
5'-GTG GGG BTG GC-3' **(FRAG. NO: 1762) (SEQ. ID NO:1775)**
5'-CCB BGB GCT BGC-3' **(FRAG. NO: 1763) (SEQ. ID NO: 1776)**
5'-TCC CTG TTT CCC CCC TTT-3' **(FRAG. NO:1140) (SEQ. ID NO:1149)**
5'-CGT TCT GCG TTT GCC TTT GGC-3' **(FRAG. NO:1141)(SEQ. ID NO:1150)**
5'-GTT TTT TGT TTG TTT TCT-3' **(FRAG. NO:1142)(SEQ. ID NO:1151)**
5'-CTC TCC GTC TTT CTT CTC C-3' **(FRAG. NO:1143) (SEQ. ID NO:1152)**
5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' **(FRAG. NO:1144) (SEQ. ID NO:1153)**
5'-GAG GGT TTC TGG CTT CCT CTC T-3' **(FRAG. NO:1145) (SEQ. ID NO:1154)**
5'-TGT CTC TCT GTC CTT TTG TT-3' **(FRAG. NO:1146) (SEQ. ID NO:1155)**
5'-TGT TGT GCG GCC TGG TGC TGC CCT GCC CCG GG-3' **(FRAG. NO:1147) (SEQ. ID NO:1156)**
5'-GTG GGA ATT TCT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA AGC ATC CTC ATG GCT CTG AAA CG-3' **(FRAG. NO: 1764) (SEQ. ID NO: 1777)**
5'-GTG GGB BTT TCT GTG GGG BTG GCB TBC BCG TBG GCB GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC BTC CTC BTG GCT CTG BBB CG-3' **(FRAG. NO:1148) (SEQ. ID NO:1157)**

<u>Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-CTCAGTGGCC CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTTACT ATGAGGCCGT GTCTGTCGTG TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCGT GTCTTTCCTT TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTTCC TTTGCTCTTG GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC-3' **(FRAG. NO: 1765) (SEQ. ID NO: 1778)**
5'-CCG TGT C-3' **(FRAG. NO: 1766) (SEQ. ID NO: 1779)**
5'-GCCCTGCC-3' **(FRAG. NO: 1767) (SEQ. ID NO: 1780)**
5'-CCG TGT CTG TCG TGT CT-3' **(FRAG. NO:1149) (SEQ. ID NO:1158)**
5'-TTCCTTTGCTCTTG-3' **(FRAG. NO:1150) (SEQ. ID NO:1159)**
5'-GTGTGTCTTTGCTCT-3' **(FRAG. NO:1151) (SEQ. ID NO:1160)**
5'-GCCCTGCCTCTCTCC-3' **(FRAG. NO:1152) (SEQ. ID NO:1161)**
5'-CT CBGTGGCCCC CBBBBGGBTG BGTBBTBCBT GCGCCBCGBT GBTCBTBTCC TTTTTBCTBT GBGG **(FRAG. NO: 1768) (SEQ. ID NO: 1781)**

<u>Human IL-6 Receptor Fragments</u>

5'-GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC TCTTCCTCCT TTTTCGTGCG TGGGCCTCCG CACGCCTCTT GCCACCTCCT GCGCAGGGCA GCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCCTC CTGCGCBGGG CBGCGCCTTG GGGCCBGCGC CGCTCCCGGC GCGGCCBGCB GGGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C-3' **(FRAG. NO: 1769) (SEQ. ID NO: 1782)**
5'-CCCGGCGC-3' **(FRAG. NO:1184) (SEQ. ID NO:1193)**
5'-GGCCBGCBGG-3' **(FRAG. NO:1186) (SEQ. ID NO:1195)**
5'-GCBGCCBGCBGCG-3' **(FRAG. NO: 1770) (SEQ. ID NO: 1783)**
5'-C GCBGCCGBCGGCC -3' **(FRAG. NO: 1771) (SEQ. ID NO: 1784)**
5'-GGGGGTGGCTTCCTGCC3'- **(FRAG. NO:1153) (SEQ. ID NO:1162)**
5'-GCGTCTCTGGGCCGTCCC-3' **(FRAG. NO:1154) (SEQ. ID NO:1163)**

5'-GTCCCTCGGCCCCGCGCCGCGCTCGGCTCCTCTCCC-3' **(FRAG. NO:1155) (SEQ. ID NO:1164)**
5'-TCTGGCCCGGCTC-3' **(FRAG. NO:1156) (SEQ. ID NO:1165)**
5'-GGGGCGGGGCGGGGCGGTGGGCGGGC-3' **(FRAG. NO:1157) (SEQ. ID NO:1166)**
5'-GGCGCTGCCCTGCGC-3' **(FRAG. NO:1158) (SEQ. ID NO:1167)**
5'-GCGGCGCTGGCCCC-3' **(FRAG. NO:1159) (SEQ. ID NO:1168)**
5'-TGCTGGCCGTCGGCTGCGCGCTGCTGGCTGCCCT-3' **(FRAG. NO:1160) (SEQ. ID NO:1169)**
5'-GCTGGCCGCGCCGGG-3' **(FRAG. NO:1161) (SEQ. ID NO:1170)**
5'-GCCTGTCCGCCTCTGCGGG-3' **(FRAG. NO:1162) (SEQ. ID NO:1171)**
5'-CGCTGTCTCCTGGC-3' **(FRAG. NO:1163) (SEQ. ID NO:1172)**
5'-TTGTCTTCCGGCTCT-3' **(FRAG. NO:1164) (SEQ. ID NO:1173)**
5'-TCTGCTGGGGTGGG-3' **(FRAG. NO:1165) (SEQ. ID NO:1174)**
5'-GCTGGGCGGCCGGCCCGGT-3' **(FRAG. NO:1166) (SEQ. ID NO:1175)**
5'-GCTGGGGCTCCTCGGGGGG-3' **(FRAG. NO:1167) (SEQ. ID NO:1176)**
5'-GGGGGCTCTTCCGG-3' **(FRAG. NO:1168) (SEQ. ID NO:1177)**
5'-GCTGTCTCCCTCCGGG-3' **(FRAG. NO:1169) (SEQ. ID NO:1178)**
5'-GCGGGGGTTTCTGGCC-3' **(FRAG. NO:1170) (SEQ. ID NO:1179)**
5'-GTGGGGGTCTTGCC-3' **(FRAG. NO:1171) (SEQ. ID NO:1180)**
5'-TGGCCTCCGGGCTCC-3' **(FRAG. NO:1172) (SEQ. ID NO:1181)**
5'-TGCTTGTCTTGCCTTCCTTC-3' **(FRAG. NO:1173) (SEQ. ID NO:1182)**
5'-TCTGGTCGGTTGTGGCTCG-3' **(FRAG. NO:1174) (SEQ. ID NO:1183)**
5'-GGGCTCCGTGGGTCCCTGGC-3' **(FRAG. NO:1175) (SEQ. ID NO:1184)**
5'-GCCCGTTTGTGTTTTGTC-3' **(FRAG. NO:1176) (SEQ. ID NO:1185)**
5'-TTTTCCCCTGGCGT-3' **(FRAG. NO:1177) (SEQ. ID NO:1186)**
5'-CCCTGTGCCCCTCTCCTCTCCTTCCTCTGCTTCTC-3' **(FRAG. NO:1178) (SEQ. ID NO:1187)**
5'-GCTCTCCTTTGTGGG-3' **(FRAG. NO:1179) (SEQ. ID NO:1188)**
5'-GCCCTCCCTGCTGCT-3' **(FRAG. NO:1180) (SEQ. ID NO:1189)**
5'-CTTGGTTTTGGGCT-3' **(FRAG. NO:1181) (SEQ. ID NO:1190)**
5'-TTTTTTCTCTTCCTCCTTTTTC-3' **(FRAG. NO:1182) (SEQ. ID NO:1191)**
5'-GTGCGTGGGCCTCC-3' **(FRAG. NO:1183) (SEQ. ID NO:1192)**
5'-GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC-3' **(FRAG. NO:1185) (SEQ. ID NO:1194)**
5'-GCBCGCCTCT TGCCBCCTCC TGCGCBGGGC BGCGCCTTGG GGCCBGCGCC GCTCCCGGCG CGGCCBGCBG GGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C-3' **(FRAG. NO:1187) (SEQ. ID NO:1196)**

<u>Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'--GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT CTGCTTCTCG CTCTCCTTTG TGGCGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC TCTTCCTCCT TTTTCGTGCG TGGGCCTCC GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCCTC CTGCGCBGGG CBGCGCCTTG GGGCCBGCGC CGCTCCCGGC GCGGCCBGCB GGGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C-3' **(FRAG. NO:1772) (SEQ. ID NO:1785)**
5'-GGGGCBGG-3' **(FRAG. NO:1773) (SEQ. ID NO:1786)**
5'-GBBGGCBG CBGGC 3' **(FRAG. NO:1774) (SEQ. ID NO:1787)**
5'-CCBGGBGCBG CCCC-3' **(FRAG. NO:1775) (SEQ. ID NO:1788)**
5'-BGGG BGBBGGCBBC-3' **(FRAG. NO:1776) (SEQ. ID NO:1789)**
5'-GCT TCT CTT TCG TTC CCG GTG GGC TCG-3' **(FRAG. NO:1188) (SEQ. ID NO:1197)**
5'-GTG GCT GTC TGT GTG GGG CGG CT-3' **(FRAG. NO:1189) (SEQ. ID NO:1198)**
5'-GTG CCT CTT TGC TGC TTT C-3' **(FRAG. NO:1190) (SEQ. ID NO:1199)**
5'-GAT TCT TTG CCT TTT TCT GC-3' **(FRAG. NO:1191) (SEQ. ID NO:1200)**
5'-CTCCTGGGGG TBCTGGGGCB GGGBBGGCBG CBGGCBBCBC CBGGBGCBGC CCCBGGGBGB BGGCBBCTGG BCCGBBGGCG CTTGTGGBGB BGGBGTTCBT BGCTGGGCTC CTGGBGGGGB GBTBGBGC-3' **(FRAG..NO:1777)(SEQ.ID NO:1790)**

Human Monocyte-derived Neutrophil Chemotactic Factor

Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT GCBCCTTCBC BCBGBGCTGC BGBBBTCBGG BBGGCTGCCB BGBGBGCCBC GGCCBGCTTG GBBGTCBTGT TTBCBCBCBG TGBGBTGGTT CCTTCCGGGC TTGTGTGCTC TGCTGTCTCT TGGTTCCTTC CGGTGGTTTC TTCCTGGCTC TTGTCCTTTC TCTTGG CCCT TGGC-3' **(FRAG. NO:1778) (SEQ. ID NO: 1791)**

5'-GGBGT BTG-3' **(FRAG. NO:1779) (SEQ. ID NO: 1792)**

5'-GCBCTGBCBT CT-3' **(FRAG. NO:1780) (SEQ. ID NO:1793)**

5'-CCG GTG G-3' **(FRAG. NO:1781) (SEQ. ID NO: 1794)**

5'-GG CCC TTG GC-3' **(FRAG. NO:1782) (SEQ. ID NO: 1795)**

5'-GCT TGT GTG CTC TGC TGT CTC T-3' **(FRAG. NO:1192) (SEQ. ID NO:1201)**

5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' **(FRAG. NO:1193) (SEQ. ID NO:1202)**

5'-TTC TCT TGG CCC TTG GC-3' **(FRAG. NO:1194) (SEQ. ID NO:1203)**

5'-GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT GCBCCTTCBC BCBGBGC-3' **(FRAG. NO:1783) (SEQ. ID NO: 1796)**

Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG TCTCTGCCCC TCCGTGCTGG TGGGGCTGGG GCTCCGGGG TCTCTGCCCC TCCGTGCCGC GTGGGGCCGC GCTCGCCGGC CCCCCCCTGC CGGGTGGGCT CCCGCCGCGC GCCGGCCTGC CGGCCCCTCG TGGGTCCTGC TGGCCGGGTC CGGGTCCCGG GGGTGGGGCG CGBGTCGGCG GCCGBGGGTC-3' **(FRAG. NO:1784) (SEQ. ID NO: 1797)**

5'-GG TGG GGC-3' **(FRAG. NO:1785) (SEQ. ID NO: 1798)**

5'-G GGG CCG -3' **(FRAG. NO:1786) (SEQ. ID NO:1799)**

5'- GGC CGG GTC CGG G-3' **(FRAG. NO:1787) (SEQ. ID NO: 1800)**

5'-TGG TGG GGC TGG GGC TCC GGG GTC TCT GCC CCT CCG TGC-3' **(FRAG.NO:1195)(SEQ.ID NO:1204)**

5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' **(FRAG. NO:1196) (SEQ. ID NO:1205)**

5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' **(FRAG. NO:1197) (SEQ. ID NO:1206)**

5'-CGC CGG CCT GCC GGC CCC TC-3' **(FRAG. NO:1198) (SEQ. ID NO:1207)**

5'-GTG GGT CCT GCT GGC CGG GTC CGG GTC CCG GGG GTG GGG-3'**(FRAG.NO:1199)(SEQ.ID NO:1208)**

5'-CGC GBG TCG GCG GCC GBG GGT C-3' **(FRAG. NO:1200) (SEQ. ID NO:1209)**

5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG TCTCTGCCCC TCCGTGC-3' **(FRAG. NO:1788) (SEQ. ID NO: 1801)**

Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG TBGBBBCTBG GBGGCCGGCC TCCBCCBGGG BCBTGGTCCT TCTTGTCCGC TGCCTCTCTG GGGTTTTCGG TCTGGGTGGG CTTTCCTCCT GGGGCTGCTG CTGGGCTCTT CTTTTTGTTT CTGGCCTGGT GCTCTCTCGT GCCCTTTCCC TTGGGTGTCT TGTTTTTGTG GCCTCCBCCB GGGBCBTG-3' **(FRAG. NO:1789) (SEQ. ID NO: 1802)**

5'-CGGGBGTGGG GG-3' **(FRAG.NO:1790) (SEQ. ID NO: 1803)**

5'-GCCBGCBCCCC-3' **(FRAG.NO:1791) (SEQ. ID NO: 1804)**

5'-C CBC CBG-3' **(FRAG.NO:1792) (SEQ. ID NO: 1805)**

5'-GGC CTC CBC CBG GGB CBT G-3' **(FRAG. NO:1201) (SEQ. ID NO:1210)**

5'-GTC CTT CTT GTC CGC TGC C -3' **(FRAG. NO:1202) (SEQ. ID NO:1211)**

5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3 **(FRAG. NO:1203) (SEQ. ID NO:1212)**

5'-GCT TTC CTC CTG GGG CTG CTG CTG-3' **(FRAG. NO:1204) (SEQ. ID NO:1213)**

5'-GGC TCT TCT TTT TGT TTC TGG CCT GGT G-3' **(FRAG. NO:1205) (SEQ. ID NO:1214)**

5'-CTC TCT CGT GCC CTT TCC-3' **(FRAG. NO:1206) (SEQ. ID NO:1215)**

5'-CTT GGG TGT CTT GTT TTT GT-3' **(FRAG. NO:1207) (SEQ. ID NO:1216**

5'-GGC CTC CBC CBG GGB CBT G-3' **(FRAG. NO:1208) (SEQ. ID NO:1217)**

5'-CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG TBGBBBCTBG GBGGCC-3' **(FRAG. NO:1793) (SEQ. ID NO: 1806)**

Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC

CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC TCTGGTCTGC CTTCGGGGGT CGT-3' **(FRAG. NO:1794) (SEQ. ID NO: 1807)**

5'-GBBGBTBCGCC-3' **(FRAG. NO:1795) (SEQ. ID NO: 1808)**

5'-CBGCCCCBG-3' **(FRAG. NO:1796) (SEQ. ID NO: 1809)**

5'-TCC CGT CTC TGG-3' **(FRAG. NO:1797) (SEQ. ID NO: 1810)**

5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' **(FRAG. NO:1209) (SEQ. ID NO:1218)**

5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' **(FRAG. NO:1210) (SEQ. ID NO:1219)**

5'-TCT GCC TTC GGG GGT CGT-3' **(FRAG. NO:1211) (SEQ. ID NO:1220)**

5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG-3' **(FRAG. NO:1798) (SEQ. ID NO: 1811)**

<u>Human Defensin 1 Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC TBGCTBGGCB GGGTGBCCBG BGBGGGC GGG TCC TCB TGG CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG BGT CTT CCC TGG T GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG AGAACTTCCT ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACTTTC TCACAGGCCT TGGCCACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC CTGCCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAGGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTTAATAA AGGAAAATTG CTTTTGAAGT AT CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTTACCT TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGCTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCCTTGGC TGGTAGATGA CCGCCGCCTC CCTGGGTCCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA ATGACCGTGT TTAACTTGAA TCACCTCTTT AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACT GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCACTGGAGA CTTGCAACAT GGCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCCTGT TGCATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC CAAGTAGAAA AAAAAACTAT GAAAGTTTTA GAGAGTAACC ATAATTTCAG CCCGATGTGA AACCATCCTA GATTTCAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGAAC AGCGTAACTG AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAAAACACA GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAAACT TGTTTGGAAA AATAACTTGA ATTCCCTGCA CATTTAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC ATTCCTTGGC TTGTATTTGG SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT CATGAGTAGC CCCAAAGATC AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT ATTTGTTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA GTGGAGGGCA ATGTCTCTAT TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAACGT GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCCAGTTC CTGAAATCCT GAGTGTTGCC TGCCAGTCGC CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT -3' **(FRAG.NO:1799) (SEQ. ID NO: 3010)**

5'-GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCCAGTTC CTGAAATCCT GAGTGTTGCC TGCCAGTCGC CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT-3' **(FRAG.NO:___) (SEQ. ID NO: 2475)**

5'-CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT
GAGCACTTGC AATCCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT
GCCATATTGG ATGCTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTTACCT TGGTTGGCGG
AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA
CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT
TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC
CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGGTAGCGA
TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG
TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG
TTGGCTTCTT CTCAGGTGTC TGTCCTTGGC TGGTAGATGA CCGCCGCCTC CCTGGGTCCT CACATGGTCT
TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA
ATGACCGTGT TTAACTTGAA TCACCTCTTT AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACT
GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCAGTGGAGA
CTTGCAACAT GGCCGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCCTGT TGCATGGAAT
AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC
CAAGTAGAAA AAAAAACTAT GAAAGTTTTA GAGAGTAACC ATAATTTCAG CCCGATGTGA AACGATCCTA
GATTTCAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGAAC AGCGTAACTG
AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAAAACACA
GGATGTGATT TTGCGGTGTG TTGAGACAAG GCAGAAAACT TGTTTGGAAA AATAACTTGA ATTCCCTGCA
CATTTAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC ATTCCTTGGC TTGTATTTGG
SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT CATGAGTAGC CCCAAAGATC
AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT ATTTGTTCTG CTTTCGCGAG
ATGTTCTCAA ATCCTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA CAGGTGGTAA
CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA GTGGAGGGCA ATGTCTCTAT
TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG
CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCTTTT AATAAAGGAA
AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG
TAGGGGGTTA GGGTGCATGG GTTGGAACGT GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG
TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG-3'
(FRAG.NO:___) (SEQ. ID NO: 2474)

5'-GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG
AGAACTTCCT ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACTTTC
TCACAGGCCT TGGCCACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC
CTGCCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAGGCCA AGTGCTGCAA GTGAGCTGGG
AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTTAATAA AGGAAAATTG
CTTTTGAAGT AT-3' **(FRAG.NO:___) (SEQ. ID NO: 2472)**

5'-CCGGGGC-3' **(FRAG.NO:1800) (SEQ. ID NO: 1813)**

5'-GG GCCTGCBGGG CC-3' **(FRAG.NO:1801) (SEQ. ID NO: 1814)**

5'-GGCBGCB BGG-3' **(FRAG.NO:1802) (SEQ. ID NO: 1815)**

5'-GGG TCC TCB TGG CTG GGG-3' **(FRAG. NO:1212) (SEQ. ID NO:1221)**

5'-GCC TGG GCC TGC BGG GCC-3' **(FRAG. NO:1213) (SEQ. ID NO:1222)**

5'-GCT CTT GCC TGG BGT GGC TC-3' **(FRAG. NO:1214) (SEQ. ID NO:1223)**

5'-GCC CBG BGT CTT CCC TGG T-3' **(FRAG. NO:1215) (SEQ. ID NO:1224)**

5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG
BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC TBGCTBGGCB GGGTGBCCBG
BGBGGGC-3' **(FRAG.NO:1803) (SEQ. ID NO: 1816)**

Human Defensin 2 Nucelic Acid and Antisense Oligonucleotide Fragments

5'-ATCCTTTAAG TCAATGGACT TTGCATCAGT CACACCATCT TTTGTTACTT TGGACTTCCC CAGCTATGTT
CAATAATTAC TGTTCTTCCC TTGGGCCCCA TTGTAATGGC TACAGCCTCG ACAAAAAGTC TACACTTTGA
AGCATTAAGG CTCCGACATC AGCACCAAAT TTTACATCTT TACCATCACT TCAAGTGAGG TGAGGAGCCA
GTAGCCTGGA CACTGGTCTC ATCTGGTGAA AGACTGTGGG TAATGGAAGC ATTTCTGTGG GGTGCTGGCA
GGACATGTGC ATGGCGAGGC AGGTCATCAG CAGCAAGTGA GAGCTGCCTC TTACTTTCTA AAGGTGACAT
AGCAAATATA CAAAAAAAAA TAAATAAATT ATTAATTTAG GTAGAGCACA TAAAGGCTTT ATTTCATATT
CCATTTCTCT GTATGCTTTC TTCACCAGGA AGAAATAGTT TTAGTGTCAG GAATGAATGA GTCTGCCCCT
CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG TGACTCCCTG GTGACTAAGC
TCCCAGTCCT GGATGCATAT TTGTTTAGCA GTTCTGACAG CATTTGACCC AGCCCTCTCT CTGCATATCC
CATCAGAACC TTCTTTTTTT TTTTTTTCTT TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCCTGTGCC
TCAGCCTCCC AAATACCTGG AATTATAGGC GTAAGCCATC ATGCCTGGCT AATTTTTGTA TTTTTCATGG
AGATGGGGTT TTGCCATGTT GGTCAAATTG GTCTCACACT CCTGACCTCA TGTGATCCAC CTGCCTCAGC
CTCCCAAACT GCTCGGATGA CAGGTGTAAG CCACCATGCT AGGCTCAGAA ATTTCCTTTT ATAAAAATGT
CATTAAGGAT CTTCGCTGCA CAATATCGTT ACCAGCTTCC TTTAAATCCA CTTCTGGCCT GCCAGGAATC

AGGTTCTTCA GAACCTGACA TTTTAAATGA AGAGGTCAGG CAGTTCATGA GGAAAGCCTC ATTGTCCCCA
TGTCTCTGTC ACTGCTGCAC CCCTGAGACA TCACAGACAT GGACACTGGG GCCTGCTTGT TTCTCAAACT
GCCCTTAGAT CGAAAGAGGG AGGAACCAGG ATGAATGCCA CTCATTTTCC CAAGAAAGGC CCTCTCCTGA
GTGCCCGGGA TGGGGCTCTG TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTTACGG AGGAAGGACA
GGGTCCTGAG AGACACCAGA GACCTCACAC AGCCCTGAAA ACATGGGGCT CCTTCATAAG TGTTTCCCAT
CACCAACAGG GAGACCACGT GGAGGCCTTG CAGCCCCACT CGGTGCTTCT CCACCAAATC CCAAGGGCAG
TGACGCTGAC GTCTGTGGAA AGCAGAGAAA GCCCTGGCTC CCAAAGCCCT GAAGTCCCTG TGGAGCTGAC
ATTCCCTGAG TGACGGTGTG AATGGAAGGA ACTCAAGTGC GGGTGGTAGG CCACCTCCTG GCCCAGGCCT
GGGTGAACTC TGAGGGGACA CATGTAGTCA CAATCCCATC CTCCCATTCT CCTTCTCAGA GGAAGGAAGT
GGGCATCCAT CTGCCTCATC TCTCTCCCGT GGGGAAGATG GGGAGTTTCA GGGGAACTTT CACATAAATT
TCACCAGCTC AGATCTCCTG TGAGGATGGG GCCCACCATG CTCCCGGTGC TGCCAGAGGC CCTGAGCCCC
TCCCAGGGTC CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA ATGTCAGAGC AATGGATAGA
ATTAGATGGA AAGAGCTCTC AATTTGACCT GAGACTGTCC CCAGATACTC AGGAAAAACA GGACGTCGCA
CAGAGTGGGC AGCAGGTGAG TGGCAGGTTA TAGGTCCTGA GTTTGAGTTT GTTCTCACGT GAGACAGACC
CAGCCCCTCA CTCCATTCAC ACACTGGGTT TTAAATGGTG CAAGATAGGA GCAATTTTCT GGTCCCAAGA
GCAGGAGGAA GGGATTTTCT GGGGTTTCCT GAGTCCAGAT TTGCATAAGA TCTCCTGAGT GTGCATTGTT
CTTTGAGGAC CATTCTCTGA CTCACCAGGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG CATTGCACCC
AATACCAGTT CTGAACTCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCCT
CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC ATGAGGGTCT TGTATCTCCT CTTCTCGTTC
CTCTTCATAT TCCTGATGCC TCTTCCAGGT GAGATGGGCC AGGGAAATAG GAGGGTTGGC CAAATGGAAG
AATGGCGTAG AAGTTCTCTG TCTCCTCTCA TTCCCCTCCA CCTATCTCTC CCTCATCCCT CTCTCTCCTT
CCTCTCTCTG TGTGTCCCCT CCATCCTTTT CTCCTGCTTC TCTCTCTTCT TCCCTCTCTC TCTTTTTTCT
GTCTTTCTTT TTCCTCTCTC CCTAGAGCAT GTCTTTCTTT CTTTCTCTTT CCTTTCTTCT ACCCACACTT
TTAGACTGAA TGCCCTATTT AATTGAACAA AGCATTGCTT CCTTCAATAG AAAAGGAGTT TGAGAACCCA
ATGGACACCT CACTCGTTCT TCTAAGCCAA TATGAAGGAG CCCAGTAGCT TGTAAATATC ATCTCTTCAC
TGCTTTCCAT GCTACAACTG CTGAGACTAT GGTTGAAACC TGTTAGGTGA CTTTTTAAAT AAAAGGCAGA
AATTTTGATT TTATCTAAAG AAAGTAGTAT AGAATGTCAT TTTCTAAATT TTTATATTTA AAGGGTAGAT
ACTGCAACCT AGAGAATTCC AGATAATCTT AAGGCCCAGC CTATACTGTG AGAACTACTG CAGCAAGACA
CTCTGCCTCC AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA
CAGGACAGGG TACAGCCCAT TGAAACCTAC TTTTAAACCT GGATGCCTAA CCTTCATTTT CTCCTTGATA
TTATGAAAAT AAAATAAAAA CCATGAAAGG ATAAAAGAGG GAGAGTGGAA GGGAAGGATG GAGAAAGGGA
AAAAGAAAAT TTGAGAGTAA ATCCTAAAAC AATTAATCTA ATAGATATCA TCTTGTGAAA TCCTCATTTT
ACCAATCTTA TTTATGAGTC CTGGGTTTTG TGAGAACAAT GGGGTTCTGA GAGGCACCAG AGACCTCATG
TTTTCCAAAA CCTAGAACAG TATAATGAAG GAAGGCGGGG AGGCAGGGAG GCAGGGAGGC AGGGAGGCAG
GGAGGCGGGC AGGTGGGGAG GGAGGGACGG AAGGAGGGAG GGAGGGAGGG AGGGAGGGAG GGAGGGATAA
AAAAAGAAGA ATGAGGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA TTACAAAATT TATTTCTATG
GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTTAAT TTCCTATTAA ACAATTTCAG TAAGTTGCAT
CTTTTTATCC CATCTCAGGT CAAATACTTA ACAGACTAAA TGATTTGAAA AAGCAAAAGT TTACTGGCTT
GTGTGTGTTA AAATGGAGGT ATGGTGGCTT TGATATTATC TTCTTGTGGT GGAGCTGAAT TCACAAGAGA
TCGTTGCTGA GCTCCTACCA GACCCCACCT GGAGGCCCCA GTCACTCAGG AGAGATCAGG GTCTTTCACA
ATCAGGTTCT ACAAAAATAA ACATCCCCCC AACCACAGCA GTGCCAGTTT CCATGTCAGA AACTTAGATC
CAAATGACTG ACTCGCGTCT CATTATCATG ATGGAAAAGC CCAGGCTTGA GAAAGAAGCC CGCTGCGGAT
TTACTCAAGG CGATACTGAC ACAGGGTTTG TGTTTTTCCA ACATGAGTTT TGAGTTCTTA CACGCTGTTT
GCTCTTTTTG TGTGTTTTTT CCCTGTTAGG TGTTTTTGGT GGTATAGGCG ATCCTGTTAC CTGCCTTAAG
AGTGGAGCCA TATGTCATCC AGTCTTTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GGTCTCCCTG
GAACAAAATG CTGCAAAAAG CCATGAGGAG GCCAAGAAGC TGCTGTGGCT GATGCGGATT CAGAAAGGGC
TCCCTCATCA GAGACGTGCG ACATGTAAAC CAAATTAAAC TATGGTGTCC AAAGATACGC AATCTTTATC
CTAGTAATTG TGGTCATTGG GTGATGTTGG TTTGGGCAGG CCATCTCTAA TATCCTTGAA ACACCTTTTT
CTGCTCTCCA GGAAGGGGTC AGGGCTGCCA CAGCGGGGCT TGGAGTGCTT TCCAGGGTCA CAGGCATCTG
TATTCTTTGG ATTCCTTGAC CTTCCCCATT TATTCCCGGC ATTTTCCTAA AACGTGTGCT TTGCTCCTCC
TGCATCCTCC CCTTGCATGC CCTCACCTAC CCCACATCTT CCCTAAAAAA AGCAAGCCCA ACTCAAAGAC
CAGTTCCCTC ATGGAATCAT AGTGGATCTG CCAAGGGAGG GGATGCCCAG TCCTCTGTTC TTCACAAGAC
TCCCTTCTTC TGGCTAAGGT TTCTTATGCA ATTAT GAATTCACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT
GGAGAAATAT ATCCTCTATC AAATTTTCAT GCCTTCAATA ATTTCTAATT CATCAGTCAG TGTTTTTCCA
TCCTTTACTG TGATGATGCC CTTTCTTCCA AACTTTTTCA TTGCATCAGA GATGATGTTA CCAATTTCTT
TGTCTCCATT TGCAGAAATT GTAGCAACCT GTGCAATTTC TTCAGGTTTG GTCACAGGTT TAGACTGCTT
TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA CCTCTCTTGA TTTCCACTGG ATTAGCACCT
TTGCTAACCT TCTGGAAGGC TTATTTGGAA ATAGAGCATA CCAGTACAGC AGCAGTGATA GTGCCATCCC
CCAGTCTCTC CATTTGTGTT ATTGGCAACA TCTTGGACAA GTTTAGCTCC AATGCTTTTA TATTTATCCT
TTAAGTCAAT TGACTTTGCA TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCCCAGC TATGTTCAAT
AATTACTGTT CTTCCCTTTG GCCCCATTGT AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA
TTAAGGCTCA GACATCAGCA CCAAATTTTA CATCTTTACC ATCACTTCAA GTGAGGTGAG GAGCCAGTAG

CCTGGACACT GGTCTCATCT GGTGAAAGAC TGTGGGTAAT GGAAGCATTT CTGTGGGGTG GTGGCAGGAC
ATGTGCATGG TGACGCAGGT CATCAGCAGC AAGTGAGAGC TGCCTCTTAC TTTCTAAAGG TGACATAGCA
AGTATACAAA AAAAAATAAA ATATTAATTT AGGCAGAGCA CATAAAGGCT TTATTTCATA TTCCATTTCT
CTGTATGCTT TCTTCACCAG GAAGAAATAG TTTTAGTGTC AGGAATGAAT GAGTCTGCCC CTCAATTCCA
GCCTGCTCAG CACACAAGGA AACAAAGCCC TGACAATCAG AGTGACTCCC TGGTGACTAA GCTCCAGTCC
TGGATGCATA TTTCTTTAGC AGTTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC CCACCAGAAC
CTTCTTTTTT TTTTTTTTTC TTTGAGACTG AGTCTTGCTC TGTCGGAAGC GATTCCCGTG CCTCAGCCTC
CCAAATACCT GGAATTATAG GCGTAAGCCA TCATGCCTGG CTAATTTTTG TATTTTTCAT GGAGATGGGG
TTTTGCCATG TTGGTCAAAT TGGTCTCACA CTCCTGACCT CATGTGATCC ACCTGCCTCA GCCTCCCAAA
GTGCTGGGAT GACAGGTGTA AGCCACCATG CTAGGCTCAG AAATTTCCTT TTATAAAAAT GTCATTAAGG
ATCTTGGCTG CACAATATCG TTACCAGCTT CCTTTAAATC CACCTCTGGC CTGCCAGGAA TCAGGGTTCT
TCAGAACCTG ACATTTTAAA TGAAGAGGTC AGGCAGGTCA TGAGGAAAGC CTCATTGTCC CCATGTCTCT
GTCACTGCTG CACCCCTGAG ACATCACAGA CATGGACACT GGGGCCTGCT TGTTTCTCAA ACTGCCCTTA
GATCGAAAGA GGGAGGAACC AGGATGAATG CCACTCATTT TCCCAAGAAA GGCCCTCTCC TGAGTGCCCG
GGATGGGGCT CTGTCCATTG CCTGGGGCCG CCAATTGCTA CTCTGGGTTA CGGAAGAAGG ACAGGGTCCT
GAGAGACACC AGAGACCTCA CACAGCCCTG AAAACATGGG GCTCCTTCAT AAGTGTTTCC CATCACCAAC
AGGGAGACCA CGTGGAGGCC TTGCAGCCCT ACTCGGTGCT TCTCCACCAA ATCCCAAGGG CAGTGACGCT
GACGTCTGTG GAAAGCAGAG AAAGCCCTGG CTCCCAAAGC CCTGAAGTCC TGTGGAGCTG ACATTCCCTG
AGTGACGGTG TGAATGGAAG GAACTCAAGT GCGGGTGGTA GGCCACCTCC TGGCCCAGGC CTGGGTGAAC
TCTGAGGGGA CACATGTAGT CACAATCCCA TCCTCCCATT CTCCTTCTCA GAGGAAGGAA GTGGGCATCC
ATCTGCCTCA TCTCTCTCCC GTGGGGAAGA TGGGGAGTTT CAGGGGAACT TTCACATAAA TTTCACCAGC
TCAGATCTCC TGTGAGGATG GGGCCCACCA TGCTCCCGGT GCTGCCAGAG GCCCTGAGCC CCTCCAGGGT
CCCTGGGTTT GAGCCAGCCC TGTATCATCC CCAGGAGCTG AATGTCCGAA CAATGGATAG AATTAGATGG
AAAGAGCTCT CAATTTGGCC TGAGACTGTC CCCAGATACT CAGGAAAAAC AGGACGTCGC ACAGAGTGGG
CAGCAGGTGA GTGGCAGGTT ATAGGTCCTG AGTTTGAGTT TGTTCTCACG TGAGACAGAC CCAGCCCCTC
ACTCCATTCA CACACTGGGT TTTAAATGGT GCAAGATAGG AGGAATTTTC TGGTCCCAAG AGCAGGAGGA
AGGGATTTTC TGGCGTTTCC TGAGTCCAGA TTTGCATAAG ATCTCCTGAG TGTGCATTGT TCTTTGAGGA
CCATTCTCTG ACTCACCAGG TAAGTGGCTG AATTCTAACC TCTGTAATGA GCATTGCACC CAATACCAGT
TCTGAACTCT ACCTGGTGAC CAGGGACCAG GACCTTTATA AGGTGGAAGG CTTGATGTCC TCCCCAGACT
CAGCTCCTGG TGAAGCTCCC AGCCATCAGC CATGAGGGTC TTGTATCTCC TCTTCTCGTT CCTCTTCATA
TTCCTGATGC CTCTTCCAGG TGAGATGGGC CAGGGAAATA GGAGGGTTGG CCAAATGGAA GAATGGCGTA
GAAGTTCTCT GTCTCCTCTC ATTCCCCTCC ACCTATCTCT CCCTCATCCC TCTCTCTCCT TCCTCTCTCT
GTGTGTCCCC TCCATCCTTT TCTCCTGCTT CTCTCTCTTC TTCCCTCTCT CTCTTTTTTT CTGTCTTTCT
TTTTCCTCTC TCCCTAGAGC ATGTCTTTCT TTCTTTCTCT TTCCTTTCTT CTACCCACAC TTTTAGACTG
AGTAGACTGA ATGCCCTATT TAATTGAACC AAGCATTGCT TCCTTCAATA GAAAAGGAGT TTGAGAACCC
AATGGACAAC TCACTCGTTC TTCTAAGCCA ATATGAAGGA GCCCAGTAGT TTGTAAATAT CATCTCTTCA
CTGCTTTCCA TGCTACAACT GCTGAGACTA TGGTTGAAAC CTGTTAGGTG ACTTTTTAAA TAAAAGGCAG
AAATTTTGAT TTTATCTAAA GAAAGTAGTA TAGAATGTCA TTTTCTAAAT TTTTATATTT AAAGAGTAGA
TACTGCAACC TAGAGAATTC CAGATAATCT TAAGGCCCAG CCTATACTGT GAGAACTACT GCAGCAGACA
CTCTGCCCCC AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA
CAGGACAGGG ACAGCCCATT GAAACCAACT TTTAAACCTG GATGCCTAAC CTTCATTTTC TCCTTGATAT
TATGAAAATA AAATAAAAAC CATGAAAGGA TAAAAGAGGG AGAGTGGAAG GGAAGGATGG AGAAAGGGAA
AAAGAAAATT TGAGAGTAAA TCCTAAAACA ATTAATCTAA TAGATATCAT CTTGTGAAAT CCTCATTTTA
CCAATCTTAT TTATGAGTCC TGGGTTTTGT GAGAACAATG GGGTTCTGAG AGGCACCAGA GACCTCATAT
TTTCCAAAAC CTAGAACAGT ATAATGAAGG AAGGAGGGAA GGAGGGAGGG AGGGAGGGAA GGAGGGAAGG
AGGGAGGGAG GGAGGGAAAC AAAAAGAAGA ATGAGGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA
TTACAAAATT TATTTCTATG GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTTAAT TTCCTATTAA
ACAATTTCAG TAACTTGCAT CTTTTTTATC CCATCTCAGA TCAAATACTT AACAGACTAA ATGATTTGAA
AAAGCAAAAG TTTACTGGCT TGTGTGTGTT AAAATGGAGG TATGGTGGCT TTGATATTAT CTTCTTGTGG
TGGAGCTGAA TTCACAAGAG ATCGTTGCTG AGCTCCTGCC AGACCCCACC TGGAGGCCCC AGTCACTCAG
GAGAGATCAG GGTCTTTCAC AATCAGGTTC TACAAAAATA AACATCCCCC AAACCACAGC AGTGCCAGTT
TCCATGTCAG AAACTTAGAT CCAAATGACT GACTCGCGTC TCATTATCAT GATGGAAAAG CCCAGGCTTG
AGAAAGAAGC CCGCTGCGGA TTTACTCAAG GCGATACTGA CACAGGGTTT GTGTTTTTCC AACATGAGTT
TTGAGTTCTT ACACGCTGTT TGCTCTTTTT GTGTGTTTTT TCCCTGTTAG GTGTTTTTGG TGGTATAGGC
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TTGGCACCTG TGGTCTCCCT GGAACAAAAT GCTGCAAAAA GCCATGAGGA GGCCAAGAAG CTGCTGTGGC
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(FRAG. NO:___) (SEQ. ID NO:3011)

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Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG CCBCCBGGBGB BTGCBGCBBG GBTGGCGBGGG TCCTCBTGGC TGGGGTCBCCT GGBGGBGGGB GBGCBGGGGG TCCTCBTGGC TGGGGTCCCT CTCTCCCGTC CT CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCCT GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTTCCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' **(FRAG. NO:1804) (SEQ. ID NO:3013)**

5'-CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCCT GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTTCCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' **(FRAG. NO:___) (SEQ. ID NO:2478)**

5'-GAATTCCCTG TAAGCCCTGT TACAGGGGCT GCACCCCAGA TACAACCTGA CCTGTGTCCA AGGCGGGCAA CTCAACCCTT AGATATTGAA TGGGTCCCAT GGCACCAATG CTTAAACACC AGCAGCCCTC ACAACCACAG ATCGTGTTTT AAGGATGAGG AGGTAGTTCT CTGGATGCAC AGGCTTCAAT CCAAATGGGC TCATGACGCC GCAGCACACA CCCAGTCTGC AGCCTGAAGA GTTGGAGCAT TGCATTCACA GAAAGCATCC AGACATGATC ATGGGCTCAG GGATACACCT GTTCTCCGAT GTGTACCAGT GAAGGATGGA AACTCCTATG CCTCCCAGAA AGCACCACTC AAGCTTTTGC TGAATGCTTC TCTGAAGGCC CACAAGGCTG AGAGGCTGTG CAACACCAGC AGTAAAGTGA ATGCCCAGAC TCCCACCTCC TTTCTTGGGT GGCCATCTGG AAAGGCCACT CCCACCCTGA TGGCTAATGC CTCAGACCAG TTCTTGGCCC AGATGATCCT AGACAATTGT TTAAGCTTAA ACTGTTCATT GGCCAAGCAA ACAGGTGATA GTACCTCTGG GGAACCACAT GCCGCGTGTA CATCCAGATC TCAGGAGAAC CCAAAAATGT CTGTTCCACA TAGCAACAGA AGCCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC ATCCCAGCTC AGCCAAATGG CTTTCATTAG TTTTTATGGT TAGACCCCAG GTCCTCGGGA CACTGCTTTA GAAACACATT CCAAATCCTC CTCTGTGTGC AGGTGGCATT CCTATCCCAA TCTCTTTGCA GGGCGTATAC TGTGATACGC AGCCAGGCTG TCCCAGAGGC CTTAAATATT CCCTTGGTGC AGGTAGTTCA GCTTAGCCAC AGCCAATGCA TCACAGGGTC AACTGTGTTA GGAGCCATTG AGAATCCATA GTTGGTTGCT GCCTGGGCCT GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC TTCCCACCAA ATTTCTCAAC TGTCCTTGCC ACCACAATTA TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC ACCTCATCCC AAAAGACCTT TAAATAGGGG AAGTCCACTT GTGCACGGCT GCTCCTTGCT ATAGAAGACC TGGGACAGAG GACTGCTGTC TGCCCTCTCT GGTCACCCTG CCTAGCTAGA GGATCTGTAA GTACTACAAA ACTTAAACTT TACACTGAGT TTTCATCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT GTGGGGCCGC CCCAGAGGGA CCCAGCGGGT GAATCCCTGC TAGGAACGTC TGTCCGGACC TCTGGTGACT GCTGGGGACG ATGGCTTCCA GCTAACTTAA TAGAGAAACT CAAGCAGTTT CCTTCTAAAT ACACATGTCA CATGTCCTGG TTGACATGTC CAGTAAGAAG ACTATCACAG GTCTTTGGAA CATTCTTTTG AGAGAAACCT ATTTAGGTCC TTGGTCTGTT TTTCAATCAG GTTGTTTGAT TTTTGCTATT GAGTTGTTGG AATTCCTTAT GTATTCAGAT ATTTGCCCCT TCTCCCATGT AGGTTTTGCA AATATTTTCT CTCATTTTCT GGGTTATCTT TTCACTCGGT TGATTGTTTC CTTTGCTGTG CAGATGCTTT AGCGTTAAAT GAAGCCACAC TTGTCTATTT TCCCTTTTAT TGCCTGTGCC TTTGGTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT CAAAAGCTTT ATCCTTCTAT ACACTTCTAG TAGTTTATGG TTTCAGTTGT TACATTTAGG TTTTCAATTC ATTCTGAGTT GATGTTCCTA CATGGTGTGA GATAAAGATT TAAATACATA CATATATAAA ATCATGAGGT AGTGTACACT ATAAATATAC AATTGTTAAT TGTTACTCAA GTCTAAGTAG AGGTGGAAAT AATAAACTTT CTTTTTTTTA CTTAAACCAC TCTGTGTCAC TGACCTGATT TCACCTTTAG CCTGATAAAA TCATTGTCCT CTCCACCCTG ATTCCTACAG GAGACTACTC ACCCCATAAC CTCAAAAACC TCTTCATGAG GATGGTAAGT CACCTGAATC CTGAAGTGAA TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC CAGAGAACAG CAGGACCCAT CTTCAGAAAA TAAGAAGCAT TTGTTCCCTG AGCCTGTTGA ATCAAAGTGC AATTTCTATT CTTTTTGGAA TGTTAAAAAG TGAATCATAA TATTTAAGCA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCAT TATTAGCTCC AACCTAGCAC AGACATTAAA GGTACAGATG TATACTAGCA TGAAACTGGG AGAACAGGAG CATTCGAGCA ACCTTGAGAC CAATGGGCCT CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA AGGTTTCTTG TCTCCGAGCC TTCTCCCAGT AGAGCTATAA ATCCAGGCTG GCTCCTCCCT CCCCACACAG CTGCTCCTGC TCTCCCTCCT CCAGGTGACC CCAGCCATGA GGACCCTCGC CATCCTTGCT GCCATTCTCC TGGTGGCCCT GCACGCCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGCTGCAG CCCCGGAGCA GATTGCAGCG GACATCCCAG AAGTGGTTGT TTCCCTTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTC CAGAGTTGGG

TCTCAGCAGT CTATGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTTCTC ATCTAGAAAT
TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA ACATCTGTGA
AATTCACTAA GTTTAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT
AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA AACTGCAGCC AAGCCTGAGG GTAAGTTCAG
GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA AGGAGAATGA GTCTCAAATT CTGTGTGACA
AGCACTGCTC TGCCTGTTTA TTCCTATCGA CTGAGGTTGT TCGTGCTACC GGCTGCAATG CAGCCAGCAT
CACCTGTCAG CTAGCATGTG ACTTCCCCGA GATTCTTTTT CTTACCCACT GCTAACTCCA TACTCAATTT
CTCATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCATTGC
AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGCAGA
AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG GGAATTGCTA TTACTCCTGT ACCTTCTGCT
CAATTTCCTT TCCTCATCTC AAATAAATGC CTTGTTACAA GATTTCTGTG TTTCCACCTC TTTAATGTGT
GATATGTGTC TGTGTCAAGA CACTTGGGAT ACACGTACCA AAACGCAAAA TCAAATTTTT GAACAATATA-3'
(FRAG. NO:___) (SEQ. ID NO:2477)

5'-GGCBGCBBGG-3' **(FRAG. NO:1805) (SEQ. ID NO:1818)**

5'-GG CTG GGG-3' **(FRAG. NO:1806) (SEQ. ID NO:1819)**

5'-GGGGTCBCC-3' **(FRAG. NO:1807) (SEQ. ID NO:1820)**

5'-GGG TCC TCB TGG CTG GGG TC-3' **(FRAG. NO:1216) (SEQ. ID NO:1225)**

5'-CCT CTC TCC CGT CCT-3' **(FRAG. NO:1217) (SEQ. ID NO:1226)**

5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG
CCBCCBGGBGB BTGGCBGCBBG GBTGGCGBGGG TCCTCBTGGC TGGGGTCBCCT GGBGGBGGGB GBGCBGG-3'
(FRAG. NO:1808) (SEQ. ID NO:1821)

Human Macrophage Inflammatory Protein-1-alpha/RANTES Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GTCTTTGTTT CTCGGCTCGT GCCCCBTCCC GGCTTCTCTC TGGTTCCGTC CTCTGTGGTG TTTGGCCCTG
CTTCCTTTTG CCTGTTGAGG GGGCAGCAGT TGGGCCCCAA AGGCCCTCTC GTTCACCTTC TGGCACGGAGTT
GCATCCCCATA GTCAAACTCT GTGGTCGTGT CATAGTCCTC TGTGGTGTTT GGAGTTTCCA TCCCGGCTTC
TCTCTGGTTC CAACGGAGB GGGGGCBGCB GTTGGGCCCC BBBGGCCCTC TCGTTCBCCT TCTGGCBCGG
BGTTGCBTCC CCBTBGTCBB BCTCTGTGGT CGTGTCBTBG TCCTCTGTGG TGTTTGGBGT TTCCBTCCCG
GCTTCTCTCT GGTTCCBBGG GB-3' **(FRAG. NO:1809) (SEQ. ID NO:1822)**

5'-GGGCC CC-3' **(FRAG. NO:1810) (SEQ. ID NO:1823)**

5'-GGGGGCBGC-3' **(FRAG. NO:1811) (SEQ. ID NO:1824)**

5'-CCCGGCTTC-3' **(FRAG. NO:1812) (SEQ. ID NO:1825)**

5'-GTC TTT GTT TCT CGG CTC GTG CC-3' **(FRAG. NO:1218) (SEQ. ID NO:1227)**

5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' **(FRAG. NO:1219) (SEQ. ID NO:1228)**

5'-GTC CTCTGT GGT GTT TGG-3' **(FRAG. NO:1220) (SEQ. ID NO:1229)**

5'-CCC TGC TTC CTT TTG CCT GTT-3' **(FRAG. NO:1221) (SEQ. ID NO:1230)**

5'-GAGGGGGCAG CAGTTGGGCC CCAAAGGCCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT CCCCATAGTC
AAACTCTGTG GTCGT-3' **(FRAG. NO:1222) (SEQ. ID NO:1231)**

5'-GTCATAGTCCTCTCTGGTGTTTGGAGTTTCCATCCCGGCTTCTCTCTGGTTCCAAGGGA-3' **(FRAG.NO:1223)(SEQ.ID NO:1232)**

5'-GBGGGGGCBG CBGTTGGGCC CCBBBGGCCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBGTC
BBBCTCTGTG GTCGTG-3' **(FRAG. NO:1224) (SEQ. ID NO:1233)**

5'-TCBTBGTCCTCTGTGGTGTTTGGBGTTTCCBTCCCGGCTTCTCTCTGGTTCCBBGGGB-3'**(FRAG. NO:1225)(SEQ. ID NO:1234)**

RANTES Antisense Oligonucleotide Fragments

5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC
BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB
CCTGTGGBGB GGCTGTCGGB GGGGGTGTGG TGTCCGCTTG GCGGTTCTTT CGGGTGTTTC TTCTCTGGGT
TGGCCTGCTG CTCGTCGTGGT CGCTCCGCTC CCGGGTTCGT CTCGCTCTGT CGCCCCTTCC TTCCTTGTCG
TGTTCCTCCC TTCCTTGCCT CT-3' **(FRAG. NO: 1813) (SEQ. ID NO: 1826)**

5'-GGGTTGGC-3' **(FRAG. NO: 1814) (SEQ. ID NO: 1827)**

5'-CGGGG CBG-3' **(FRAG. NO: 1815) (SEQ. ID NO: 1828)**

5'-CCCGGGTTCG-3' **(FRAG. NO: 1816) (SEQ. ID NO: 1829)**

5'-GGGTGTGGTG-3' **(FRAG. NO: 1817) (SEQ. ID NO: 1830)**

5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC
BGBTGCBGGB GCGC-3' **(FRAG. NO:1226) (SEQ. ID NO:1235)**

5'-BGBGGGCBGTB GCBBTGBGGB TGBCBGCGBG GCGTGCCGCG GBGBCCTTCB TGGTBCCTGT GGBGBGGCTG
TCGGBGG-3' **(FRAG. NO:1227) (SEQ. ID NO:1236)**

5'-GGGTGTGGTGTCCGCTTGGCGGTTCTTTCGGGTGTTTCTTCTCTGGGTTGGCCTGCTGCTCGTCGTGGTC-3' **(FRAG. NO:1228) (SEQ. ID NO:1237)**

5'-GCTCCGCTCCCGGCGTTCGTCTCGCTCTGTCGCCCCTTCCTTCCTTGTCGTGTTCCTCCCTTCCTTGCCTCT-3' **(FRAG. NO:1229) (SEQ. ID NO:1238)**
5'-GGGTGTGGTGTCCG-3' **(FRAG. NO:1230) (SEQ. ID NO:1239)**
5'-CTTGGCGGTTCTTTCGGGTG-3' **(FRAG. NO:1231) (SEQ. ID NO:1240)**
5'-TTTCTTCTCTGGGTTGGC-3' **(FRAG. NO:1232) (SEQ. ID NO:1241)**
5'-CTGCTGCTCGTCGTGGTC-3' **(FRAG. NO:1233) (SEQ. ID NO:1242)**
5'-GCTCCGCTCCCGGCGTTC-3' **(FRAG. NO:1234) (SEQ. ID NO:1243)**
5'-GTCTCGCTCTGTCGCCC-3' **(FRAG. NO:1235) (SEQ. ID NO:1244)**
5'-CTTCCTTCCTTGTC-3' **(FRAG. NO:1236) (SEQ. ID NO:1245)**
5'-GTGTTCCTCCCTTCCTTGCCTCT-3' **(FRAG. NO:1237) (SEQ. ID NO:1246)**
5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GG-3' **(FRAG. NO:1818) (SEQ. ID NO:1831)**

<u>Human Muscarinic Acetylcholine Receptor HM1* Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-GCTGCCCGGC GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC TTCGTCCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCCT CGGGGTCCCG GGGCTTCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGTG GCTBGGTGGG GC-3'**(FRAG. NO:1819)(SEQ. ID NO: 1832)**
5'-GGTGGGGC-3' **(FRAG. NO:1820) (SEQ. ID NO: 1833)**
5'-GCCCGGCGGGG-3' **(FRAG. NO:1821) (SEQ. ID NO: 1834)**
5'-CGG GGC TTC TGG CCC-3' **(FRAG. NO:1822) (SEQ. ID NO: 1835)**
5'-GTT CBT GGT GGC TBG GTG GGG C-3' **(FRAG. NO:1238) (SEQ. ID NO:1247)**
5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' **(FRAG. NO:1239) (SEQ. ID NO:1248)**
5'-GCT CCC GTG CTC GGT TCT CTG TCT CCC GGT-3' **(FRAG. NO:1240) (SEQ. ID NO:1249)**
5'-CCC CCT TGG CCT GGC GTC TCG G-3' **(FRAG. NO:1241) (SEQ. ID NO:1250)**
5'-GCC TTC GTC CTC TTC CTC TTC TTC CTT CC-3' **(FRAG. NO:1242) (SEQ. ID NO:1251)**
5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' **(FRAG. NO:1243) (SEQ. ID NO:1252)**
5'-CGG GGC TTC TGG CCC TTG CC-3' **(FRAG. NO:1244) (SEQ. ID NO:1253)**
5'-GTT CAT GGT GGC TAG GTG GGG C-3' **(FRAG. NO: 1245) (SEQ. ID NO:1254)**

<u>Human Muscarinic Acetylcholine Receptor HM3* Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-GGG GTG GGT BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TGGCG CTG GCG GGG GGG CCT CCTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG CCGGG GTG GGT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT GCA GGG G-3' **(FRAG. NO:1823) (SEQ. ID NO:1836)**
5'-CCC GGG CGG-3' **(FRAG. NO:1824) (SEQ. ID NO:1837)**
5'-G GCG GGG GGG CC-3' **(FRAG. NO:1825) (SEQ. ID NO:1838)**
5'-CCC GGG CCG CC-3' **(FRAG. NO: 1826) (SEQ. ID NO: 1839)**
5'-GG CCG TGT-3' **(FRAG. NO:1827) (SEQ. ID NO:1840)**
5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' **(FRAG. NO:1246) (SEQ. ID NO:1255)**
5'-GTT GGC CBT GTT GGT TGC C-3' **(FRAG. NO:1247) (SEQ. ID NO:1256)**
5'-TCT TGG TGG TGC GCC GGG C-3' **(FRAG. NO:1248) (SEQ. ID NO:1257)**
5'-GCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3'**(FRAG.NO:1249)(SEQ.ID NO:1258)**
5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' **(FRAG. NO:1250) (SEQ.ID NO:1259)**
5'-GCG CTG GCG GGG GGG CCT CCT CC-3' **(FRAG. NO:1251) (SEQ. ID NO:1260)**
5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' **(FRAG. NO:1252) (SEQ. ID NO:1261)**
5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' **(FRAG. NO:1253) (SEQ. ID NO:1262)**
5'-GGG CCC GCG GCT GCB GGG G-3' **(FRAG. NO:1254) (SEQ. ID NO:1263)**
5'-TTG CCT GTC TGC TTC GTC-3' **(FRAG. NO:1255) (SEQ. ID NO:1264)**
5'-CTT TGC GCT CCC GGG CCG CC-3' **(FRAG. NO:1256) (SEQ. ID NO:1265)**
5'-GGG GTG GGT AGG CCG TGT CTG GGG-3' **(FRAG. NO:1257) (SEQ. ID NO:1266)**
5'-GTT GGC CAT GTT GGT TGC C-3' **(FRAG. NO:1258) (SEQ. ID NO:1267)**
5'-GGG CCC GCG GCT GCA GGG G-3' **(FRAG. NO:1259) (SEQ. ID NO:1268)**

<u>Human Fibronectin* Antisense Oligonucleotide Fragments</u>

5'-CGG TTT CCT TTG CGG TC TTG GCC CGG GCT CCG GGT G CCC GCC CGC CCG CCG GCC GCC GC CCC GCC GGG CTG TCC CCG CCC CGC CCC GGC CCG GGG CGC GGG GG CGG CCC TCC CGC CCC TCT GG GCC GGC GCG GGC GTC GG CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C GCC TGC CTC TTG CTC TTCTGC GTC

CGC TGC CTT CTC CC CTC TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGC CCT TCC GTG GTG C TGT TGT CTC TTC TGC CCT C GGT GTG CTG GTG CTG GTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG GCC TCT TCG GGT GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT TGT CTG GGG TGG TGC TCC TCT CCC TTT CCC TGC TGG CCG TTT GT CCT GTT TTC TGT CTT CCT CT TTC CTC CTC TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT GTG GGC TTT CCC TGG TCC GGT CTT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC C TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' **(FRAG. NO:1828) (SEQ. ID NO: 1841)**

5'-GGCCCGGGC-3' **(FRAG. NO:1829) (SEQ. ID NO: 1842)**

5'-GCCGGCGCGGGCG 3' **(FRAG. NO:1830) (SEQ. ID NO:1843)**

5'-GCCTGGGCTGGCC-3' **(FRAG. NO:1831) (SEQ. ID NO: 1844)**

5'-GGGGG TGGCCG-3' **(FRAG. NO:1832) (SEQ. ID NO: 1845)**

5'-GG GGG TGG CCG TTG TGG GCG G-3' **(FRAG. NO:1833) (SEQ. ID NO: 1846)**

5'-CGG TTT CCT TTG CGG TC-3' **(FRAG. NO:1260)(SEQ. ID NO:1269)**

5'-TTG GCC CGG GCT CCG GGT G-3' **(FRAG. NO:1261)(SEQ. ID NO:1270)**

5'-CCC GCC CGC CCG CCG GCC GCC GC-3' **(FRAG. NO:1262)(SEQ. ID NO:1271)**

5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' **(FRAG. NO:1263)(SEQ. ID NO:1272)**

5'-GGC CCG GGG CGC GGG GG-3' **(FRAG. NO:1264)(SEQ. ID NO:1273)**

5'-CGG CCC TCC CGC CCC TCT GG-3' **(FRAG. NO:1265)(SEQ. ID NO:1274)**

5'-GCC GGC GCG GGC GTC GG-3' **(FRAG. NO:1266)(SEQ. ID NO:1275)**

5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' **(FRAG. NO:1267)(SEQ. ID NO:1276)**

5'-GCC TGC CTC TTG CTC TTC-3' **(FRAG. NO:1268)(SEQ. ID NO:1277)**

5'-TGC GTC CGC TGC CTT CTC CC-3' **(FRAG. NO:1269)(SEQ. ID NO:1278)**

5'CTC TCC TCG GCC GTT GCC TGT GC-3' **(FRAG. NO:1270)(SEQ. ID NO:1279)**

5'-TGT CCG TCC TGT CGC CCT TCC GTG GTG C-3' **(FRAG. NO:1271)(SEQ. ID NO:1280)**

5'-TGT TGT CTC TTC TGC CCT C-3' **(FRAG. NO:1272)(SEQ. ID NO:1281)**

5'-GGT GTG CTG GTG CTG GTG GTG GTG-3' **(FRAG. NO:1273)(SEQ. ID NO:1282)**

5'-CCT CTG CCC GTG CTC GCC-3' **(FRAG. NO:1274)(SEQ. ID NO:1283)**

5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' **(FRAG. NO:1275)(SEQ. ID NO:1284)**

5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' **(FRAG. NO:1276)(SEQ. ID NO:1285)**

5'-CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT-3' **(FRAG. NO:1277)(SEQ. ID NO:1286)**

5'- TGT CTG GGG TGG TGC TCC TCT CCC-3' **(FRAG. NO:1278)(SEQ. ID NO:1287)**

5'-TTT CCC TGC TGG CCG TTT GT-3' **(FRAG. NO:1279)(SEQ. ID NO:1288)**

5'-CCT GTT TTC TGT CTT CCT CT-3' **(FRAG. NO:1280)(SEQ. ID NO:1289)**

5'-TTC CTC CTG TTT CTC CGT-3' **(FRAG. NO:1281)(SEQ. ID NO:1290)**

5'-TTG GCT TGC TGC TTG CGG GGC TGT CTC C-3' **(FRAG. NO:1282)(SEQ. ID NO:1291)**

5'-CTT GCC CCT GTG GGC TTT CCC-3' **(FRAG. NO:1283)(SEQ. ID NO:1292)**

5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' **(FRAG. NO:1284)(SEQ. ID NO:1293)**

5'-GCC CTT CTT GGT GGG CTG-3' **(FRAG. NO:1285)(SEQ. ID NO:1294)**

5'-GCT CGT CTG TCT TTT TCC TTC C-3' **(FRAG. NO:1286)(SEQ. ID NO:1295)**

5'-TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T-3' **(FRAG. NO:1287)(SEQ. ID NO:1296)**

5'-TGC CTC TGC TGG TCT TTC-3' **(FRAG. NO:1288)(SEQ. ID NO:1297)**

<u>Human Interleukin-1 (IL-1) Nucleic Acid and antisense Oligocnucleotide Fragments</u>

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GGTCATCTGC ATGAAAAAGC AAATCATAGT GTGACAGCAT TAGGGATACA AAAAGATATA GAGAAGGTAT
ACATGTATGG TGTAGGTGGG GCATGTACAA AAAGATGACA AGTAGAATCG GGATTTATTC TAAAGAATAG
CCTGTAAGGT GTCCAGAAGC CACATTCTAG TCTTGAGTCT GCCTCTACCT GCTGTGTGCC CTTGAGTACA
CCCTTAACCT CCTTGAGCTT CAGAGAGGGA TAATCTTTTT ATTTTATTTT ATTTTATTTT GTTTTGTTTT
GTTTTGTTTT GTTTTATGAG ACAGAGTCTC ACTCTGTTGC CCAGGCTGGA GTGCAGTGGT ACAATCTTGG
CTTACTGCAT CCTCCACCTC CTGAGTTCAA GCGATTCTCC TTCCTCAGTC TCCTGAATAG CTAGGATTAC
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GAGCCACCAC GCCTGGCCCA GAGAGGGATG ATCTTTAGAA GCTCGGGATT CTTTCAAGCC CTTTCCTCCT
CTCTGAGCTT TCTACTCTCT GATGTCAAAG CATGGTTCCT GGCAGGACCA CCTCACCAGG CTCCCTCCCT
CGCTCTCTCC GCAGTGCTCC TTCCAGGACC TGGACCTCTG CCCTCTGGAT GGCGGCATCC AGCTACGAAT
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CCAACTCAAT TCCCCCAGAG CCAAAGCCCT TTAAAGGTAG AAGGCCCAGC GGGGAGACAA AACAAAGAAG
GCTGGAAACC AAAGCAATCA TCTCTTTAGT GGAAACTATT CTTAAAGAAG ATCTTGATGG CTACTGACAT
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GGGCTAGTGT TATCACCATC ACCATTTTAC CTAAGTAGCT CTGTTGCTCG GCCACAGTGA GCAGTAATAG
ACCTGAAGCT GGAACCCATG TCTAATAGTG TCAGGTCCAG TGTTCTTAGC CACCCCACTC CCAGCTTCAT
CCCTACTGGT GTTGTCATCA GACTTTGACC GTATATGCTC AGGTGTCCTC CAAGAAATCA AATTTTGCCA
CCTCGCCTCA CGACGCCTGC CCTTCTGATT TTATACCTAA ACAACATGTG CTCCACATTT CAGAACCTAT
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CGGGACTCAC AGCAAAAAAG CTTGGTGATG TCTGGTCCAT ATGAACTGAA AGCTCTCCAC CTCCAGGGAC
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GAACTTATAT CTCTCCGCTG TAACGGGCAA AAGTTTCAAG TGCGGTGAAC CCATCATTAG CTGTGGTGAT
CTGCCTGGCA TCGTGCCACA GTAGCCAAAG CCTCTGCACA GGAGTGTGGG CAACTAAGGC TGCTGACTTT
GAAGGACAGC CTCACTCAGG GGGAAGCTAT TTGCTCTCAG CCAGGCCAAG AAAATCCTGT TTCTTTGGAA
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CCTGAAACAG TTCTGGTGCC TGATTTCTGG CAGAAGTACA GCTTCACCTC TTTCCTTTCC TTCCACATTG
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GTGTCTTAGG CCAAGGAACC TCACTGTGGG TTCCCACAGA GGCTACCAAT TACATGTATC CTACTCTCGG
GGCTAGGGGT TGGGGTGACC CTGCATGCTG TGTCCCTAAC CACAAGACCC CCTTCTTTCT TCAGTGGTGT
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GACTTAAAGG GTCCCATTAT CACGTCCACT CCACTCCCAA AATCACCACC ACTATCACCT CCAGCTTTCT
CAGCAAAAGC TTCATTTCCA AGTTGATGTC ATTCTAGGAC CATAAGGAAA AATACAATAA AAAGCCCCTG
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CCCACTCCTC ATTGCTGAGT GCTGCAAGTA CCTAGAAATA TCCTTGGCCA CCGAAGACTA TCCTCCTCAC
CCATCCCCTT TATTTCGTTG TTCAACAGAA GGATATTCAG TGCACATCTG GAACAGGATC AGCTGAAGCA
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CAAGCGCTAT GTACTAGGAG CTGGGAGTAC AGAGATGAGA ACAGTCACAA GTCCCTCCTC AGATAGGAGA
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GAGCCCAGGA GTTCAAGACC AGCCTGGGCA ACATAGTGAG ACTCCCATCT CTACAAAAAA TAAATAAATA
AATAAAACAA TCAGCCAGGC ATGCTGGCAT GCACCTGTAG TCCTAGCTAC TTGGGAAGCT GACACTGGAG
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5'-ACAAACCTTT TCGAGGCAAA AGGCAAAAAA GGCTGCTCTG GGATTCTCTT CAGCCAATCT TCAATGCTCA
AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA TGGCTTATTA CAGTGGCAAT
GAGGATGACT TGTTCTTTGA AGCTGATGGC CCTAAACAGA TGAAGTGCTC CTTCCAGGAC CTGGACCTCT
GCCCTCTGGA TGGCGGCATC CAGCTACGAA TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCCGC
GTCAGTTGTT GTGGCCATGG ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT
GACCTGAGCA CCTTCTTTCC CTTCATCTTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG
CTTATGTGCA CGATGCACCT GTACGATCAC TGAACTGCAC GCTCCGGGAC TCACAGCAAA AAAGCTTGGT

GATGTCTGGT CCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA TGGAGCAACA AGTGGTGTTC TCCATGTCCT TTGTACAAGG AGAAGAAAGT AATGACAAAA TACCTGTGGC CTTGGGCCTC AAGGAAAAGA ATCTGTACCT GTCCTGCGTG TTGAAAGATG ATAAGCCCAC TCTACAGCTG GAGAGTGTAG ATCCCAAAAA TTACCCAAAG AAGAAGATGG AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA GCTGGAATTT GAGTCTGCCC AGTTCCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCCTGGGAG GGACCAAAGG CGGCCAGGAT ATAACTGACT TCACCATGCA ATTTGTGTCT TCCTAAAGAG AGCTGTACCC AGAGAGTCCT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GGCAGAAAGG GAACAGAAAG GTTTTTGAGT ACGGCTATAG CCTGGACTTT CCTGTTGTCT ACACCAATGC CCAACTGCCT GCCTTAGGGT AGTGCTAAGA GGATCTCCTG TCCATCAGCC AGGACAGTCA GCTCTCTCCT TTCAGGGCCA ATCCCAGCCC TTTTGTTGAG CCAGGCCTCT CTCACCTCTC CTACTCACTT AAAGCCCGCC TGACAGAAAC CAGGCCACAT TTTGGTTCTA AGAAACCCTC CTCTGTCATT CGCTCCCACA TTCTGATGAG CAACCGCTTC CCTATTTATT TATTTATTTG TTTGTTTGTT TTGATTCATT GGTCTAATTT ATTCAAAGGG GGCAAGAAGT AGCAGTGTCT GTAAAAGAGC CTAGTTTTTA ATACCTATGG AATCAATTCA ATTTGGACTG GTGTGCTCTC TTTAAATCAA GTCCTTTAAT TAAGACTGAA AATATATAAG CTCAGATTAT TTAAATGGGA ATATTTATAA ATGAGCAAAT ATCATACTGT TCAATGGTTC TCAAATAAAC TTCACT-3' **(FRAG. NO:_)(SEQ. ID NO:2513)**

5'-CTGGCAGGAG TAGCAGCTGC CCCTTGGCGC GACTGCTGGA GCCGCGAACT AGAGAAACAC AGACACGCCT CATAGAGCAA CGGCGTCTCT CGGAGCGTGG AGCCCGCCAA GCTCGAGCTG AGCTTTCGCT TGCCGTCCAC CACTGCCCAC ACTGTCGTTT GCTGCCATCG CAGACCTGCT GCTGACTTCC ATCCCTCTGG ATCCGGCAAG GGCCTGCGAT TTTCACAATG TCAAGATTTA CCGTATATCC CTGTTTGTTT GGATACACCA GTGACGTCCA CTTCTAGAAG ACAAAGTTAT ATTACTTAAA CAACCAAAGA TATGAAACTA TCCATGAAGA ACAATATTAT CAATACACAG CAGTCTTTTG TAACCATGCC CAATGTGATT GTACCAGATA TTGAAAAGGA AATACGAAGG ATGGAAAATG GAGCATGCAG CTCCTTTTCT GAGGATGATG ACAGTGCCTC TACATCTGAA GAATCAGAGA ATGAAAACCC TCATGCAAGG GGTTCCTTTA GTTATAAGTC ACTCAGAAAG GGAGGACCAT CACAGAGGGA GCAGTACCTG CCTCGTGCCA TTGCCATTTT TAATGTGAAC AACAGCGACA ATAAGGACCA GGAACCAGAA GAAAAAAAGA AAAAGAAAAA AGAAAAAGAAG AGCAAGTCAG ATGATAAAAA CGAAAATAAA AACGACCCAA AGAAGAAGAT GGAAAAGCGA-3' **(FRAG. NO:_)(SEQ. ID NO:2514)**

5'-ATGGCCAAAG TTCCAGACAT GTTTGAAGAC CTGAAGAACT GTTACAGTGA AAATGAAGAA GACAGTTCCT CCATTGATCA TCTCTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT GGCCCACTCC ATGAAGGCTG CATGGATCAA TCTCTGTCTC TGAGTATCTC TGAAACCTCT AAAACATCCA AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TAGCAACCAA CGGGAAGGTT CTGAAGAAGA GACGGTTGAG TTTAAGCCAA TCCATCACTG ATGATGACCT GGAGGCCATC GCCAATGACT CAGAGGAAGA AATCATCAAG CCTAGGTCAG CACCTTTTAG CTTCCTGAGC AATCTGAAAT ACAACTTTAT GAGGATCATC AAATACGAAT TCATCCTGAA TGACGCCCTC AATCAAAGTA TAATTCGAGC CAATGATCAG TACCTCACGG CTGCTGCATT ACATAATCTG GATGAAGCAG TGAAATTTGA CATCGGTGCT TATAAGTCAT CAAAGGATGA TGCTAAAATT ACCGTGATTC TAAGAATCTC AAAAACTCAA TTGTATGTGA CTGCCCAAGA TGAAGACCAA CCAGTGCTGC TGAAGGAGAT GCCTGAGATA CCCAAAACCA TCACAGGTAG TGAGACCAAC CTCCTCTTCT TCTGGGAAAC TCACGGCACT AAGAACTATT TCACATCAGT TGCCCATCCA AACTTGTTTA TTGCCACAAA GCAAGACTAC TGGGTGTGCT TGGCAGGGGG GCCACCCTCT ATCACTGACT TTCAGATACT GGAAAACCAG GCGTAGGTCT GGAGTCTCAC TTGTCTCACT TGTGCAGTGT TGACAGTTCA TATGTACCAT GTACATGAAG AAGCTAAATC CTTTACTGTT AGTCATTTGC TGAGCATGTA CTGAGCCTTG TAATTCTAAA TGAATGTTTA CACTCTTTGT AAGAGTGGAA CCAACACTAA CATATAATGT TGTTATTTAA AGAACACCCT ATATTTTGCA TAGTACCAAT CATTTTAATT ATTATTCTTC ATAACAATTT TAGGAGGACC AGAGCTACTG ACTATGGCTA CCAAAAAGAC TCTACCCATA TTACAGATGG GCAAATTAAG GCATAAGAAA ACTAAGAAAT ATGCACAATA GCAGTTGAAA CAAGAAGCCA CAGACCTAGG ATTTCATGAT TTCATTTCAA CTGTTTGCCT TCTGCTTTTA AGTTGCTGAT GAACTCTTAA TCAAATAGCA TAAGTTTCTG GGACCTCAGT TTTATCATTT TCAAAATGGA GGGAATAATA CCTAAGCCTT CCTGCCGCAA CAGTTTTTTA TGCTAATCAG GGAGGTCATT TTGGTAAAAT ACTTCTCGAA GCCGAGCCTC AAGATGAAGG CAAAGCACGA AATGTTATTT TTTAATTATT ATTTATATAT GTATTTATAA ATATATTTAA GATAATTATA ATATACTATA TTTATGGGAA CCCCTTCATC CTCTGAGTGT GACCAGGCAT CCTCCACAAT AGCAGACAGT GTTTTCTGGG ATAAGTAAGT TTGATTTCAT TAATACAGGG CATTTTGGTC CAAGTTGTGC TTATCCCATA GCCAGGAAAC TCTGCATTCT AGTACTTGGG AGACCTGTAA TCATATAATA AATGTACATT AATTACCTTG AGCCAGTAAT TGGTCCGATC TTTGACTCTT TTGCCATTAA ACTTACCTGG GCATTCTTGT TTCATTCAAT TCCACCTGCA ATCAAGTCCT ACAAGCTAAA ATTAGATGAA CTCAACTTTG ACAACCATAG ACCACTGTTA TCAAAACTTT CTTTTCTGGA ATGTAATCAA TGTTTCTTCT AGGTTCTAAA AATTGTGATC AGACCATAAT GTTACATTAT TATCAACAAT AGTGATTGAT AGAGTGTTAT CAGTCATAAC TAAATAAAGC TTGCAAGTGA GGGAGTCATT TCATTGGCGT TTGAGTCAGC AAAGAAGTCA AG-3' **(FRAG. NO:_)(SEQ. ID NO:2515)**

5'-AGCTGCCAGC CAGAGAGGGA GTCATTTCAT TGGCGTTTGA GTCAGCAAAG AAGTCAAGAT GGCCAAAGTT

CCAGACATGT TTGAAGACCT GAAGAACTGT TACAGTGAAA ATGAAGAAGA CAGTTCCTCC ATTGATCATC
TGTCTCTGAA TCACAAATCC TTCTATCATG TAAGCTATGG CCCACTCCAT GAAGGCTGCA TGGATCAATC
TGTGTCTCTG AGTATCTCTG AAACCTCTAA AACATCCAAG CTTACCTTCA AGGAGAGCAT GGTGGTAGTA
GCAACCAACG GGAAGGTTCT GAAGAAGAGA CGGTTGAGTT TAAGCCAATC CATCACTGAT GATGACCTGG
AGGCCATCGC CAATGACTCA GAGGAAGAAA TCATCAAGCC TAGGTCATCA CCTTTTAGCT TCCTGAGCAA
TGTGAAATAC AACTTATGA GGATCATCAA ATACGAATTC ATCCTGAATG ACGCCCTCAA TCAAAGTATA
ATTCGAGCCA ATGATCAGTA CCTCACGGCT GCTGCATTAC ATAATCTGGA TGAAGCAGTG AAATTTGACA
TGGGTGCTTA TAACTCATCA AAGGATGATG CTAAAATTAC CGTGATTCTA AGAATCTCAA AAACTCAATT
GTATGTGACT GCCCAAGATG AAGACCAACC AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAAACCATC
ACAGGTAGTG AGACCAACCT CCTCTTCTTC TGGGAAACTC ACGGCACTAA GAACTATTTC ACATCAGTTG
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GGAGGACCAG AGCTACTGAC TATGGCTACC AAAAAGACTC TACCCATATT ACAGATGGGC AAATTAAGGC
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CATTTCAACT GTTTGCCTTC TGCTTTTAAG TTGCTGATGA ACTCTTAATC AAATAGCATA AGTTTCTGGG
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TATGGGAACC CCTTCATCCT CTGAGTGTGA CCAGGCATCC TCCACAATAG CAGACAGTGT TTTCTGGGAT
AAGTAAGTTT GATTTCATTA ATACAGGGCA TTTTGGTCCA AGTTGTGCTT ATCCCATAGC CAGGAAACTC
TGCATTCTAG TACTTGGGAG ACCTGTAATC ATATAATAAA TGTACATTAA TTACCTTGAG CCAGTAATTG
GTCCGATCTT TGACTCTTTT GCCATTAAAC TTACCTGGGC ATTCTTGTTT CATTCAATTC CACCTGCAAT
CAAGTCCTAC AAGCTAAAAT TAGATGAACT CAACTTTGAC AACCATGAGA CCACTGTTAT CAAAACTTTC
TTTTCTGGAA TGTAATCAAT GTTTCTTCTA GGTTCTAAAA ATTGTGATCA GACCATAATG TTACATTATT
ATCAACAATA GTGATTGATA GAGTGTTATC AGTCATAACT AAATAAAGCT TGCAACAAAA TTCTCTG-3' **(FRAG. NO:_)(SEQ. ID NO:2515)**

Human Interleukin-1 Receptor (IL-1 R) Nucleic Acids and Anti-sense Oligonucleotide Fragments

5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC
TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA
GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG
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TCTGCTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC
CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAAATGTC
CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA AATTTTAACC
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TCACTTACTC GTACACGATG TGGCCCTGGA AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT
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CTGTGATCAT TTCCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAGGT
GTTTCTGGGA ACCCGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA CATAGAGAGC
GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTCAGA AAATAATGAG AACTACATTG
AAGTGCCATT GATTTTTGAT CCTGTCACAA GAGAGGATTT GCACATGGAT TTTAAATGTG TTGTCCATAA
TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCCTG GGGCATTGTG
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CGCGGCGCGG CCGGGAGGAG CCGAGCGCGC CGGGCGCGGC GTGGGGGCGC CGGCTGCCCC GCGCGCCCAG
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CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA CGGCCGTCCG TCCAGGTAGA
CGCACCCTCT GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG GCCTTCTCCA
AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTTCTTCTC TGGAGGCTGA
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CCTCTTAACC CAAATGAACA CAAAGGCACT ATAACTTGGT ATAAAGATGA CAGCAAGACA CCTGTATCTA
CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT TTGGTTTGTT CCTGCTAAGG TGGAGGATTC
AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG
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GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAAAAATGA AAATAATGAG TTACCTAAAT TACAGTGGTA
TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA AAGATAGGCT CATCGTGATG
AATGTGGCTG AAAAGCATAG AGGGAACTAT ACTTGTCATG CATCCTACAC ATACTTGGGC AAGCAATATC
CTATTACCCG GGTAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC
AGCTAATGAG ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG
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ATTACAGTGT GGAAAATCCT GCAAACAAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA TATCGGAAAT
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ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA
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GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTTGTGT TTAAAGTCTT GCCTGAGGTC TTGGAAAAAC
AGTGTGGATA TAACCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA
TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG
GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAGGA TGGAATTAAA GTTGTCCTGC
TTGAGCTGGA GAAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAA TTCATTAAGC AGAAACATGG
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AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA GCCACTAAGG
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CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAACTA
TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3’ **(FRAG NO:_)(SEQ. ID NO:2520)**

5’-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC
TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA
GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG
CCCCCAGGTG CCCTACTGGT TGTGGGCCTC TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC
TCTGCTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC
CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAAATGTC
CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA AATTTTAACC
TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAACT GACGTGAAGA
TTCAATGGTA CAACGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC
TCACTTACTC GTACACGATG TGGCCCTGGA AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT
GAAGGCCAGC AATACAACAT CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTC
CTGTGATCAT TTCCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAGGT
GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA CATAGAGAGC
GCCTACCCGG GAGCCCGCGT GACCGAGGGG CCACGCCAGG AATATTCAGA AAATAATGAG AACTACATTG
AAGTGCCATT GATTTTTGAT CCTGTCACAA GAGAGGATTT GCACATGGAT TTTAAATGTG TTGTCCATAA
TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCCTG GGGCATTGTG
CTGGCCCCAC TTTCACTGGC CTTCTTGGTT TTGGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA
CTGGAAAAGC AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA
TAAATGGAAT GAAATAATTC AAACACAAAA AAAAAAAAAA AAAAAAAA-3’ **(FRAG. NO:_)(SEQ. ID NO:2518)**

5’-GCCGGAGCCG ACTCGGAGCG CGCGGCGCGG CCGGGAGGAG CCGAGCGCGC CGGGCGCGGC GTGGGGGCGC
CGGCTGCCCC GCGCGCCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGCACCGTAG CACTCCTCGC
TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA
CGGCCGTCCG TCCAGGTAGA CGCACCCTCT GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT
AAAAGACAAG GCCTTCTCCA AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG
ATTTCTTCTC TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT TTTAGTGTCA TCTGCAAATG
AAATTGATGT TCGTCCCTGT CCTCTTAACC CAAATGAACA CAAAGGCACT ATAACTTGGT ATAAAGATGA
CAGCAAGACA CCTGTATCTA CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT TTGGTTTGTT
CCTGCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA
AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACTTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA
ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAAAAATGA AAATAATGAG
TTACCTAAAT TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA
AAGATAGGCT CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAACTAT ACTTGTCATG CATCCTACAC
ATACTTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA
AGGCCTGTGA TTGTGAGCCC AGCTAATGAG ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT
GTAATGTCAC CGGCCAGTTG AGTGACATTG CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA
CCCAGTGCTA GGGGAAGACT ATTACAGTGT GGAAAATCCT GCAAACAAAA GAAGGAGTAC CCTCATCACA
GTGCTTAATA TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC AAGAATACAC

ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA TAATTGTGTG TTCTGTTTTC ATCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCCTG CTATGATTTT CTCCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTTGTGT TTAAAGTCTT GCCTGAGGTC TTGCAAAAAC AGTGTGGATA TAAGCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAGGA TGGAATTAAA GTTCTCCTGC TTGAGCTGGA GAAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCGC TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAAGA CAAGGTTCTG GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA GCCACTAAGG AGAAACTGCA AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTGC CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAACTA TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3' **(FRAG. NO:_)(SEQ. ID NO:2519)**

Human Interleukin-8* Fragments Antisense Oligonucleotide Fragments

5'-GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBTCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC TTGGBGTCBT GTTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT GTGCTCTGCT GTCTCTG TTC CTTCCGGTGG TTTCTTCCTG GCTCTTGTCC TTTCTCTTGG CCCTTGGCCC-3' **(FRAG. NO:1834) (SEQ. ID NO:1847)**

5'-G CTC CGG-3' **(FRAG. NO:1835) (SEQ. ID NO:1848)**

5'-CBBGBBTBGC-3' **(FRAG. NO:1836) (SEQ. ID NO:1849)**

5'-CBCBC BGTGBGGTGC-3' **(FRAG. NO:1837) (SEQ. ID NO:1850)**

5'-BCCBBBGCBT CBBGBBTBGC-3' **(FRAG. NO:1838) (SEQ. ID NO:1851)**

5'-GCCBBGBGBG CCBCGGCCBGC-3' **(FRAG. NO:1839) (SEQ. ID NO:1852)**

5'-GTG CTC CGG TGG CTT TTT-3' **(FRAG. NO:1289)(SEQ. ID NO:1298)**

5'-GCT TGT GTG CTC TGC TGT CTC TG-3' **(FRAG. NO:1290)(SEQ. ID NO:1299)**

5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' **(FRAG. NO:1291)(SEQ. ID NO:1300)**

5'-TTC TCT TGG CCC TTG GCC C-3' **(FRAG. NO:1292)(SEQ. ID NO:1301)**

5'-GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBTCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC TTGGBGTCBT GTTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT-3' **(FRAG. NO:1840) (SEQ. ID NO:1853)**

Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTC BTCBBBBTCC CBCBTCTGTG GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG TGGCTCGGTG CTTCTGCCCC TGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC CTCTTTCTCT TTGTTCGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTCC-3' **(FRAG.NO:1841)(SEQ. ID NO:1854)**

5'-CBGGGGC-3' **(FRAG. NO:1842) (SEQ. ID NO:1855)**

5'-GCBGGTGGC-3' **(FRAG. NO:1843) (SEQ. ID NO:1856)**

5'-GCGGCGCTC-3' **(FRAG. NO:1844) (SEQ. ID NO:1857)**

5'-TGGCTCGGTGCTTCTGCCCC **(FRAG. NO:1293)(SEQ. ID NO:1302)**

5'-TGTTGTTGCGGCGCTC **(FRAG. NO:1294)(SEQ. ID NO:1303)**

5'-GGTTGGTGTGGCCCCTG **(FRAG. NO:1295)(SEQ. ID NO:1304)**

5'-TGGTGCTTCGTTTCC **(FRAG. NO:1296)(SEQ. ID NO:1305)**

5'-CCCTCTTTCTCTTTGTTC **(FRAG. NO:1297)(SEQ. ID NO:1306)**

5'-GGGGGTTCTTGTGGC **(FRAG. NO:1298)(SEQ. ID NO:1307)**

5'-GGGCTGCTTGTCTCGTTCC **(FRAG. NO:1299)(SEQ. ID NO:1308)**

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGG-3' **(FRAG. NO:1845) (SEQ. ID NO:1858)**

5'-B CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTC BTCBBBBTCC CBCBTCTGTG GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG-3' **(FRAG. NO:1846) (SEQ. ID NO:1859)**

Interleukin-11 (IL-11) Nucleic Acid and Antisnese Oligonucleotide Fragments

5'-GCTCAGGGCA CATGCCTCCC CTCCCCAGGC CGCGGCCCAG CTGACCCTCG GGGCTCCCCC GGCAGCGGAC AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA ACTGTGTTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC

ACCTGGCCCC CCTCGAGTTT CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT
CTCCTGGCGG ACACGCGGCA GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC
TGGATTCCCT GCCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC
AAGGCTGCGA GCGGACCTAC TGTCCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCAGG TGGCTCTTCC
CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG GCTGCTGCGC CGGCTGCAGC
TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCGCTGG CGCCCCCCTC
CTCAGCCTGG GGGCGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC
GTGAGGGGAC TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG
CCAGATCTTA TTTATTTATT TATTTCAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCCC GCCATTATCT
CCCCCTAGTT AGACACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATTT
CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG GGACTGGGGT CCCGGATTCT
TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT CTAGGCCTGG GCAGGAACAT
ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT
TGTACAAAAA TGTGAGAAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC
CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT
CCCCAAGTCC CTCCTGCTGT CTTCCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC
CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT
CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC
TTCCCTTCCA CTCCCTCTTC CTCCTGCCTC CACCTCTCCA GGCCCCTGTC TTGTCCCTCC GTCCGGCCTT
TCTCTGCCTT TCCGTCCTCC TGCCTCCCCA TCTCTCTCTG CTAGTCCTGT CCAGCCGGAC CCCCACCCAC
AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG
ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC
CTCCTCCGAG CGCGGCGGCG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA
GGGTGAGTCA GGATGTGTCA GGCCGGCCCT CCCCTGCCGC CTGCCCCCCG CCCGCCCGCC CCAGGCCCCC
TATATAACCC CCCAGGCGTC CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC
TCCCCAGCCG CGGGCCCAGC TGACCCTCGG GGCTCCCCCG GCAGCGGACA GGGAAGGGTT AAAGGCCCCC
GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCATGGGG
AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGCTGAGT
CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG
AGATGGGCAG AGACAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG
GCCAGACAGG GCCCGAGAGG AGCGAGACGC GAGACCGAGC AGGGGCAGGG ACGCAGGGAC TGGTGCCGGG
AGGGAGGTGA CCCCCATCGA CCCAGGCCCC AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG
CAGAGAGGCT CCGCAGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG TAGCGACCCC
AGCCGGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGGAGAGCCG GGCAGATGCG GCCGACGGAG
GCGCGGACAG ACCCACGGCT GGCGGGCCCG GGGGGCGGGC TGGGGGTGTG CGAGGCGCGG GCGGCCGGGG
AGCGCTGATT GGCTGGCGGG TGGCCGGGTG GGCGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG
ACCCCCGCGC CCCCGGCGCC CCCCGCGCCC CCCGCCGCCA GCTCTCCCGC TCCCGGCGCC CGGCCGGGCC
ATGGCTCTGC CCCTCTCCGC CCAGGTGCGC TGCGGCCCGG GCTTCTGCCG CCCACCCGGC GGGCTCCTGG
GAGGGCGTCT AAGGGGTCTC CCGTGGGAGA GGTCCGTGTC TCCCGGACTC CGTCCTGGGC TTTTGGCTCC
TTCCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGGG GAGGGGGCAG GTTCTGGCCT GTGCCTCCCC
CACCATCCGC GCCCCGGGGC CCAGATTCCG GCGTCCGGGG GCGGACGGGA GACGCCCGGG CCGCGTCTGC
TCCGACGGGC GGGCCAGCCA GAGCCAGGGA GGGAGAGGGA AGCCCGCCTG GCCCTGCGAC CTGCCCGCGG
GCGTTCCACC CTGGGACTTA AGACCTCCAG CTCCATCCTC CCTAAGGCCG GGAGTCCAGG CCCCAGACCC
TCCTCCCCGA GACCCAGGAG TCCAGACCCC AGGCCTTCCT CCCTCAGACC TAGGAGTCCA GGCCCCCAGC
CTCTCCTCCC TCAGACCCAG GAGGAGTCCA GACCCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC
AGGCCCTCCT CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCTTATC CTGCCCCCAG GTGTTTGCCG
CCTGGTCCTG GTCGTGCTGA GCCTGTGGCC AGATACAGCT GTCGCCCCTG GGCCACCACC TGGCCCCCCT
CGAGTTTCCC CAGACCCTCG GGCCGAGCTG GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA
CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG
GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTC TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG
GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT
TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA

TGAGTGCAGG GGCACTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
GCAGTGAAGG GGGCGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG
CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
GGGCAGGTGG CTCTTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCGAC TGGACCGGCT
GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCCTGGCC
CCAAAATCCT GTGCCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA
CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG TAACAGCCCC GCTCTGAGAC CCTGACCCTA
ACAGTCCTGC TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA
CCCCCAAATC CTGCCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA
AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC
TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC
ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTCGGGAGT TCAAGACCAG
CCAGACCAAC ATGGTGAAAC CCTGTCTCTA CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT
GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG
CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACTCCC TCTCTCTCAA AAAAAAAAAA
AAAAAAAAAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA
TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG
CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG
AAAACCCTGA CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC
CCAAAGCCCT GAGACCAGAA GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA
ATTCCAACTT CTAGCTCTGA GACTCCAGCC CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT
CTCTAAGACT TCACCCTTGA GATCCAGGGC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT
GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG GCCAAGGCAG
AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC TTAATTATTA
TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT
TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA
CTTCAGGTGC ACACTGCCAC ACCCGGATAA TTTTTTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTTG
CCCAGGCTGG TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC
AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG
ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA ACCGAGATGC CAGCCCTGAC
TCCACAGACT TCACCCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCCT GACTCCAGCC TCCATTTTCG
GAACCCCACA GCCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT
GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCCTGCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC
TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCCGGACC CGCCGGCGCC
CCCGCTGGCG CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCACG CCATCCTGGG GGGGCTGCAC
CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC
ACCACCGTCC TTCCAAAGCC AGATCTTATT TATTTATTTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG
ATCCCCCCGC CATTATCTCC CCCTAGTTAG AGACAGTCCT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT
ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG
ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCATCT
AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA
AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT
GTCATACATA TCCACTTGAG GGCGATTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG
CAGGTGGAGG GGAGACCTCC ATTCAGGTGG AGGTCCCGAG TGGGCGGGGC AGCGACTGGG AGATGGGTCG
GTCACCCAGA CAGCTCTGTG GAGGCAGGGT CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT
GTTTGTTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT
GCAACCTCCA CCTCCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCCGA TTAGCTGGGA TCACAGGTGT
GCACCACCAT GCCCAGCTAA TTATTTATTT CTTTTGTATT TTTAGTAGAG ACAGGGTTTC ACCATGTTGG
CCAGGCTGGT TTCCAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA
GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCACCCT
GTGATCAACA GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA
GCAAACTGGA AACAATCTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC

CACCCAGCCG CCCCGAGCAG GGACTGTCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
AGATATCCTG ACATTGGCCA GGCATGGTGG CTCACGCCTG TAATCCTGGC ACTTTGGGAG GACGAAGCGA
GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCCTGTCT CAAAAAAGAA
AGAATGATGT CCTGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT
TCTTTCTATA TATGGATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC
CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT
TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTTAGA ATAACAGAAT
ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG
GGCTGTGCAC-3' **(FRAG. NO:_)(SEQ. ID NO:2523)**

5'-GCTCAGGGCA CATGCCTCCC CTCCCCAGGC CGCGGCCCAG CTGACCCTCG GGGCTCCCCC GGCAGCGGAC
AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA
ACTGTGTTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC
ACCTGGCCCC CCTCGAGTTT CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT
CTCCTGGCGG ACACGCGGCA GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC
TGGATTCCCT GCCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC
AAGGCTGCGA GCGGACCTAC TGTCCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCAGG TGGCTCTTCC
CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG GCTGCTGCGC CGGCTGCAGC
TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCGCTGG CGCCCCCCTC
CTCAGCCTGG GGGGGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC
GTGAGGGGAC TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG
CCAGATCTTA TTTATTTATT TATTTCAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCCC GCCATTATCT
CCCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATTT
CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG GGACTGGGGT CCCGGATTCT
TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT CTAGGCCTGG GCAGGAACAT
ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT
TGTACAAAAA TGTGAGAAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC-3' **(FRAG. NO:_)(SEQ. ID NO:2521)**

5'-CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT
CCCCAAGTCC CTCCTGCTGT CTTCCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC
CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT
CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC
TTCCCTTCCA CTCCCTCTTC CTCCTGCCTC CACCTCTCCA GGCCCCTGTC TTGTCCCTCC GTCCGGCCTT
TCTCTGCCTT TCCGTCCTCC TGCCTCCCCA TCTCTCTCTG CTAGTCCTGT CCAGCCGGAC CCCCACCCAC
AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG
ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC
CTCCTCCGAG CGCCGCGGCG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA
GGGTGAGTCA GGATGTGTCA GGCCGGCCCT CCCCTGCCGC CTGCCCCCCG CCCGCCCGCC CCAGGCCCCC
TATATAACCC CCCAGGCGTC CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC
TCCCCAGCCG CGGCCCCAGC TGACCCTCGG GGCTCCCCCG GCAGCGGACA GGGAAGGGTT AAAGGCCCCC
GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCATGGGG
AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGCTGAGT
CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG
AGATGGGCAG AGAGAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG
GCCAGACAGG GCCCGAGAGG AGCGAGACGC GAGACCGAGC AGGGGCAGGG ACGCAGGGAC TGGTGCCGGG
AGGGAGGTGA CCCCCATCGA CCCAGGCCCC AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG
CAGAGAGGCT CCGGAGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG TAGCGACCCC
AGCCGGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGGAGAGCCG GGCAGATGCG GCCGACGGAG
GCGCGGACAG ACCGACGGCT GGCGGGCCCG GGGGGCGGGC TGGGGGTGTG CGAGGCGCGG GCGGCCGGGG
AGCGCTGATT GGCTGGCGGG TGGCCGGGTG GGCGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG
ACCCCCGCGC CCCCGGCGCC CCCCGCGCCC CCCGCCGCCA GCTCTCCCGC TCCCGGCGCC CGGCCGGGCC
ATGGCTCTGC CCCTCTCCGC CCAGGTGCGC TGCGGCCCGG GCTTCTGCCG CCCACCCGGC GGGCTCCTGG
GAGGGCGTCT AAGGGGTCTC CCGTGGGAGA GGTCCGTGTC TCCCGGACTC CGTCCTGGGC TTTTGGCTCC
TTCCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGGG GAGGGGGCAG GTTCTGGCCT GTGCCTCCCC
CACCATCCGC GCCCCGGGGC CCAGATTCCG GCGTCCGGGG GCGGACGGGA GACGCCCGGG CCGCGTCTGC
TCCGACGGGC GGGGCAGCCA GAGCCAGGGA GGGAGAGGGA AGCCCGCCTG GCCCTGCGAC CTGCCCGCGG
GCGTTCCACC CTGGGACTTA AGACCTCCAG CTCCATCCTC CCTAAGGCCG GGAGTCCAGG CCCCAGACCC
TCCTCCCCGA GACCCAGGAG TCCAGACCCC AGGCCTTCCT CCCTCAGACC TAGGAGTCCA GGCCCCCAGC
CTCTCCTCCC TCAGACCCAG GAGGAGTCCA GACCCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC
AGGCCCTCCT CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCTTATC CTGCCCCCAG GTGTTTGCCG
CCTGGTCCTG GTCCTGCTGA GCCTGTGGCC AGATACAGCT GTCGCCCCTG GGCCACCACC TGGCCCCCCT

CGAGTTTCCC CAGACCCTCG GGCCGAGCTG GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA
CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG
GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTC TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG
GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT
TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA
TGAGTGCAGG GGCACTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
GCAGTGAAGG GGGCGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG
CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
GGGCAGGTGG CTCTTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCGAC TGGACCGGCT
GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCCTGGCC
CCAAAATCCT GTGCCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA
CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG TAACAGCCCC GCTCTGAGAC CCTGACCCTA
ACAGTCCTGC TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA
CCCCCAAATC CTGCCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA
AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC
TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC
ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTCGGGAGT TCAAGACCAG
CCAGACCAAC ATGGTGAAAC CCTGTCTCTA CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT
GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG
CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACTCCC TCTCTCTCAA AAAAAAAAAA
AAAAAAAAAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA
TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG
CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG
AAAACCCTGA CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC
CCAAAGCCCT GAGACCAGAA GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA
ATTCCAACTT CTAGCTCTGA GACTCCAGCC CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT
CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT
GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG GCCAAGGCAG
AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC TTAATTATTA
TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT
TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA
CTTCAGGTGC ACACTGCCAC ACCCGGATAA TTTTTTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTTG
CCCAGGCTGG TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC
AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG
ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA ACCGAGATGC CAGCCCTGAC
TCCACAGACT TCACCCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCCT GACTCCAGCC TCCATTTTCG
GAACCCCACA GCCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT
GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCCTGCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC
TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCCGGACC CGCCGGCGCC
CCCGCTGGCG CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCACG CCATCCTGGG GGGGCTGCAC
CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC
ACCACCGTCC TTCCAAAGCC AGATCTTATT TATTTATTTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG
ATCCCCCCGC CATTATCTCC CCCTAGTTAG AGACAGTCCT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT
ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG
ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCATCT
AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA
AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT
GTCATACATA TCCACTTGAG GGCGATTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG
CAGGTGGAGG GGAGACCTCC ATTCAGGTGG AGGTCCCGAG TGGGCGGGGC AGCGACTGGG AGATGGGTCG
GTCACCCAGA CAGCTCTGTG GAGGCAGGGT CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT
GTTTGTTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT
GCAACCTCCA CCTCCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCCGA TTAGCTGGGA TCACAGGTGT
GCACCACCAT GCCCAGCTAA TTATTTATTT CTTTTGTATT TTTAGTAGAG ACAGGGTTTC ACCATGTTGG
CCAGGCTGGT TTCCAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA
GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCACCCT
GTGATCAACA GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA
GCAAACTGGA AACAATCTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC
CACCCAGCCG CCCCGAGCAG GGACTGTCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
AGATATCCTG ACATTGGCCA GGCATGGTGG CTCACGCCTG TAATCCTGGC ACTTTGGGAG GACGAAGCGA
GTGGATCACT GAACTCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCCTGTCT CAAAAAAGAA
AGAATGATGT CCTCACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT
TCTTTCTATA TATGGATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC

CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTTAGA ATAACAGAAT ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG GGCTGTGCAC-3' (FRAG. NO:_) (SEQ. ID NO:2522)

Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GCGGTCCBGCCBTGGGTCTG GGGGCTGGG CTGCBGGCTC CGGGCGGGCG GGTGCGGGCT GCGTGCTGGG GGCTGCCCCG CAGGCCCTGC GGTCCBGCCB TGGGTCTGGG GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGGCTGCG TGCTGGGGGC TGCCCCGCAG GCCCTGC-3' **(FRAG. NO:1847) (SEQ. ID NO: 1860)**

5'-GBGCBGG BBG-3' **(FRAG. NO:1848) (SEQ. ID NO: 1861)**

5'-GCCBCBGCBGCBGC-3' **(FRAG. NO:1849) (SEQ. ID NO: 1862)**

5'-GGG TGC GGG C-3' **(FRAG. NO:1850) (SEQ. ID NO: 1863)**

5'-GGT CCB GCC BTG GGT CTG GG-3' **(FRAG. NO:1300)(SEQ. ID NO:1309)**

5'-GGC TGG GCT GCB GGC TCC GG-3' **(FRAG. NO:1301)(SEQ. ID NO:1310)**

5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' **(FRAG. NO:1302)(SEQ. ID NO:1311)**

5'-GGC TGC CCC GCA GGC CCT GC-3' **(FRAG. NO:1303)(SEQ. ID NO:1312)**

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GC-3' **(FRAG. NO:1851) (SEQ. ID NO: 1864)**

Human Tumor Necrosis Factor α Antisense Oligonucleotide Fragments

5'-GCBCCGCCTG GBGCCCTGGG GCCCCCCTGT CTTCTTGGGG BGCGCCTCCT CGGCCBGCTC CBCGTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGBGB GBGGGGCTGG TCCTCTGCTG TCCTTGCTGG TGCTCBTGGT GTCCTTTCCG CCCTGGGGCC CCCCTGTCTT CTTGGGGCCT CTTCCCTCTG GGGGCCGTCT CTCTCCCTCT CTTGCGTCTC TCTCTTTCTC TCTCTCTCTT CCCCTTTCCC GCTCTTTCTG TCTCGGTGTC TGGTTTTCTC TCTCCGCTGG CTGCCTGTCT GGCCTGCGCT CTTGGCCTGT GCTGTTCCTC CTCCGGTTCC TGTCCTCTCT GTCTGTCGCC CCCTCTGGGG TCTCCCTCTG GGTGGTGGTC TTGTTGCTTG GGCTGGGCTC CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCGTCT GCTGGCGCTG GTCCTCTGCTGTC CTTGCTGGTG CTCBTGGTGT CCTTTCCGCC CTGGGGCCCC CCTGTCTTCT TGGGGCCTCT TCCCTCTGGG GGCCGTCTC TCTCCCTCTC TTGCGTCTCT CTCTTTCTCT CTCTCTCTTC CCCTTTCCCG CTCTTTCTGT CTCGGTGTCT GGTTTTCTCT CTCCGCTGGC TGCCTGTCTG GCCTGCGCTC TTGGCCTGTG CTGTTCCTCC TCCGGTTCCT GTCCTCTCTG TCTGTCGCCC CCTCTGGGGT CTCCCTCTGG CGTGGTGGTC TTGTTGCTTG GGCTGGGCTC CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCGTCT GCTGGC-3' **(FRAG.NO:1852)(SEQ.ID NO:1865)**

5'-GGGGCCCCCC-3' **(FRAG. NO:1853) (SEQ. ID NO:1866)**

5'- GGG GGC CG TCT-3' **(FRAG. NO:1854) (SEQ. ID NO:1867)**

5'-CCBGGGGBGB GBGGGGCTGG-3' **(FRAG. NO:1855) (SEQ. ID NO:1868)**

5'-GCBCCGCCTG GBGCCCTGGG GCCCCCCTGT CTTCTTGGGG BGCGCCTCCT CGGCCBGCTC CBCGTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGBGB GBGGG-3' **(FRAG. NO:1304) (SEQ. ID NO:1313)**

5'-GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' **(FRAG. NO:1305) (SEQ. ID NO:1314)**

5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC GCT GBG GGB GCG TCT GCT GGC-3' **(FRAG.NO:1306)(SEQ.ID NO:1315)**

5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' **(FRAG. NO:1655) (SEQ. ID NO:1664)**

5'-GTG CTC BTG GTG TCC TTT CC-3' **(FRAG. NO:1656)(SEQ. ID NO:1665)**

5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' **(FRAG. NO:1657)(SEQ. ID NO:1666)**

5'-CCT CTT CCC TCT GGG GGC CG-3' **(FRAG. NO:1658)(SEQ. ID NO:1667)**

5'-TCT CTC TCC CTC TCT TGC GTC TCT C-3' **(FRAG. NO:1659)(SEQ. ID NO:1668)**

5'-TCT TTC TCT CTC TCT CTT CCC C-3' **(FRAG. NO:1660)(SEQ. ID NO:1669)**

5'-TTT CCC GCT CTT TCT GTC TC-3' **(FRAG. NO:1661)(SEQ. ID NO:1670)**

5'-GGT GTC TGG TTT TCT CTC TCC-3' **(FRAG. NO:1662)(SEQ. ID NO:1671)**

5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' **(FRAG. NO:1663)(SEQ. ID NO:1672)**
5'-GGC CTG TGC TGT TCC TCC-3' **(FRAG. NO:1664)(SEQ. ID NO:1673)**
5'-TCC GGT TCC TGT CCT CTC TGT CTG TC-3' **(FRAG. NO:1665)(SEQ. ID NO:1674)**
5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' **(FRAG. NO:1666)(SEQ. ID NO:1675)**
5'-GTG GTG GTC TTG TTG CTT-3' **(FRAG. NO:1667)(SEQ. ID NO:1676)**
5'-GGG CTG GGC TCC GTG TCT C-3' **(FRAG. NO:1668)(SEQ. ID NO:1677)**
5'-CBG TGC TCB TGG TGT CC-3' **(FRAG. NO:1669)(SEQ. ID NO:1678)**
5'-GCT GBG GGB GCG TCT GCT GGC-3' **(FRAG. NO:1670)(SEQ. ID NO:1679)**

Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTCGGTBGBC GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CCTGCGCGCC GBGBTCBCCTG CBGGGBGBBG TBGGCTTGCB GCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBCGGGCTG TGTGTGBBGG CGBGCTGGGC CCCGTCTGCT GCTCCTCGTG CCGCCTCGTC CTTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCCGG TGGTGGGGCG CGCGCGCTCG CGTCGCTCCG GCTCTTCTTT CCCGGCTCCGT CGGCCCGGGG GCCTTGGTCT CCCTCGTCCT TCBTGGTBCC G-3' **(FRAG. NO:1856) (SEQ ID NO: 1869)**
5'-GCB GCBGGBC-3' **(FRAG. NO:1857) (SEQ ID NO: 1870)**
5'-CCCGGCTCCG-3' **(FRAG. NO:1858) (SEQ ID NO: 1871)**
5'-CGGCCCGGGG GCC-3' **(FRAG. NO:1859) (SEQ ID NO:1872)**
5'-CB CGCGG-3' **(FRAG. NO:1860) (SEQ ID NO: 1873)**
5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' **(FRAG. NO:1307)(SEQ. ID NO:1316)**
5'-CCT CGT CCT TCA TGG TAC CGT CGG TGT GGT GGC-3' **(FRAG. NO:1308)(SEQ. ID NO:1317)**
5'-CTC GGG TGG GCC GGT GGT G-3' **(FRAG. NO:1309)(SEQ. ID NO:1318)**
5'-GGG CGC GCG CGC TCG CGT-3' **(FRAG. NO:1310)(SEQ. ID NO:1319)**
5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGG CCT TGG TCT C-3' **(FRAG.NO:1311)(SEQ.ID NO:1320)**
5'-CCT CGT CCT TCB TGG TBC CG-3' **(FRAG. NO:1312)(SEQ. ID NO:1321)**
5'-CTCGGTBGBC GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CCTGCGCGCC GBGBTCBCCTG CBGGGBGBBG TBGGCTTGCB GCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBCGGGCTG TGTGTGBBGG CGBGCTGG-3' **(FRAG.NO:1861) (SEQ ID NO:1874)**

Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-BCCGGCGGBG CCGCCBGGGT GGBCTGGGBG TGGGTTTCTC CCCGCCGTTC TCBCCCBCCG CGCTGBGCTC BGCGCCTBBG BCTGCTGTTT CTGGBGCTCC TTGGCBBGCC BCBBBCBGCB GBGBGBBBBT CBTGBGCBBB TBBTCCBTTC TGBBBBBBBG GGBTCBBBBB CCTCCCGTTC CCCGTTCGCC TGGCGCGCGC TGCGGGTTCC TCGTGGGTTT CTCCCCGCCG TTCTCCGGTC TGTTGCCTTT GTGGGCTTCT TGTCTTTTTG GCTGTTCTTT TCCTGCTTGG CGTCTTTTCC TTTCTTTGTG CTCGGTTGTG GGTCCGCTGG TCCTTTGCCC TGTGTGTTTC TGCTGCCCGT TCGCCTGGCG CGCGCTGCGG GTTCCTCGTG GGTTTCTCCC CGCCGTTCTC CGGTCTGTTG CCTTTGTGGG CTTCTTGTCT TTTTGGCTGT TCTTTTCCTG CTTGGCGTCT TTTCCTTTCT TTGTGCTCGG TTGTGGGTCC GCTGCTCCTT TGCCCTGTGT GTTTCTGCTG-3' **(FRAG. NO:1862) (SEQ. ID NO:1875)**
5'-CCGGCGGBG CCGCCBGGGT GGBC-3' **(FRAG. NO:1863) (SEQ. ID NO:1876)**
5'-CCGCCBGGG-3' **(FRAG. NO:1864) (SEQ. ID NO:1877)**
5'-GGCGCGCGC-3' **(FRAG. NO:1865) (SEQ. ID NO:1878)**
5'-GTGGGTCCGC-3' **(FRAG. NO:1866) (SEQ. ID NO:1879)**
5'-CCCGTTCGCCTGGCGC-3' **(FRAG. NO:1313)(SEQ. ID NO:1322)**
5'-GCGCTGCGGGTTCCTC-3' **(FRAG. NO:1314)(SEQ. ID NO:1323)**
5'-GTGGGTTTCTCCCCGCCGTTCTC-3' **(FRAG. NO:1315)(SEQ. ID NO:1324)**
5'-CGGTCTGTTGCCTTTGTGGG -3' **(FRAG. NO:1316)(SEQ. ID NO:1325)**
5'-CTTCTTGTCTTTTTGGCT-3' **(FRAG. NO:1317)(SEQ. ID NO:1326)**
5'-GTTCTTTTCCTGCTTGGC-3' **(FRAG. NO:1318)(SEQ. ID NO:1327)**
5'-GTCTTTTCCTTTCTT-3' **(FRAG. NO:1319)(SEQ. ID NO:1328)**
5'-TGTGCTCGGTTGTGGGTC-3' **(FRAG. NO:1320)(SEQ. ID NO:1329)**
5'-CGCTGGTCCTTTGCC-3' **(FRAG. NO:1321)(SEQ. ID NO:1330)**
5'-CTGTGTGTTTCTGCTG-3' **(FRAG. NO:1322)(SEQ. ID NO:1331)**
5'-CCCGTTCGCCTGGCGC-3' **(FRAG. NO:1323)(SEQ. ID NO:1332)**
5'-GCGCTGCGGGTTCCTC-3' **(FRAG. NO:1324)(SEQ. ID NO:1333)**
5'-GTGGGTTTCTCCCCGCCGTTCTC-3' **(FRAG. NO:1325(SEQ. ID NO:1334)**
5'-CGGTCTGTTGCCTTTGTGGG-3' **(FRAG. NO:1326)(SEQ. ID NO:1335)**
5'-CTTCTTGTCTTTTTGGCT-3' **(FRAG. NO:1327)(SEQ. ID NO:1336)**
5'-GTTCTTTTCCTGCTTGGC-3' **(FRAG. NO:1328)(SEQ. ID NO:1337)**
5'-GTCTTTTCCTTTCTT-3' **(FRAG. NO:1329)(SEQ. ID NO:1338)**
5'-TGTGCTCGGTTGTGGGTC-3' **(FRAG. NO:1330)(SEQ. ID NO:1339)**

5'-CGCTGGTCCTTTGCC-3' **(FRAG. NO:1331)(SEQ. ID NO:1340)**
5'-CTGTGTGTTTCTGCTG-3' **(FRAG. NO:1332)(SEQ. ID NO:1341)**

Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGCGCC CTGTCGGGCG GGBBGCCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC BGCGCBBCCB GGGCGCGTCC GCBCBGBCTT GGBGGCGGCT GCBTGCTGCT BCCTGCTCGGGCG GGBBGCCTCCG GTGGCCGCCG CGCGTCCGGT GGCCGCCGCG CCTCTCTCCT CTCCCCGTGG CCCTGTCGGG CGGGTCCTGC CGTCCTGTCT CCTTTTCTTT TGCTGTCTTG TCTTCCCGTC TCTGCTTT-3' **(FRAG. NO: 1867) (SEQ. ID NO: 1880)**
5'-CGGGCG GGBBGCC-3' **(FRAG. NO: 1868) (SEQ. ID NO: 1881)**
5'-CGGGCGGG-3' **(FRAG. NO: 1869) (SEQ. ID NO: 1882)**
5'-CCGCBCBGBC-3' **(FRAG. NO: 1870) (SEQ. ID NO: 1883)**
5'-GCGTCCGGTGGCCGCCGC-3' **(FRAG. NO:1333)(SEQ. ID NO:1342)**
5'-GCCTCTCTCCTCTCCCC-3' **(FRAG. NO:1334)(SEQ. ID NO:1343)**
5'-GTGGCCCTGTCGGGCGGG-3' **(FRAG. NO:1335)(SEQ. ID NO:1344)**
5'-TCCTGCCGTCCTGTCTCCTTT-3' **(FRAG. NO:1336)(SEQ. ID NO:1345)**
5'-TCTTTTGCTGTCTTGT-3' **(FRAG. NO:1337)(SEQ. ID NO:1346)**
5'-CTTCCCGTCTCTGCTTT-3' **(FRAG. NO:1338)(SEQ. ID NO:1347)**
5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGC-3' **(FRAG. NO: 1871) (SEQ. ID NO: 1884)**
5'-GCCCTGTCGG GCGGGBBGCC TCTCTCCTCT CCCCBGBTCC GCGBCBGGCC GCBGGCBBGB BCCBGCGCB BCCBGGGCGC GTCCGCBCBG BCTTGGBGGC GGCTGCBTGC TGCTBCCTGC TCCBGBBGCG TCCGGTGGCC GCCGC-3' **(FRAG. NO: 1872) (SEQ. ID NO: 1885)**

Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GTCTGTCCTC CCCGTCTCCT CCCACTGCTT CTCCCGGGGG CTTCCCCGGC TTCGGGTGGC CGGTGTCCCG GGCTCCGGCG CGGCGGCGGC TTCGGCTGCG GGTGGGTGGC GCGGGCTGCC GGGTCCGCGC GGCGCCTGGG CCCTTGTGCT GCTTTTTGCT TGTTCCGTTC TGGCTGCTCC GGTCTGTGTT GTGGTTGTTT TGTTTCTTCT TGGGTGTGGG CCTTGCGGTT TTGGCTGTGG GCCCTTTGGG GCCTTGGCTT CTGGCTCGTC TGTCCTCCCC GTCTCCTCCC ACTGCTTCT CCCGGGGGCT TCCCCGGCTT CGGGTGGCCG GTGTCCCGGG CTCCGGCGCG GCGGCGGCTT CGGCTGCGGG TGGGTGGCGC GGGCTGCCGG GTCCGCGCGG CGCCTGGGCC CTTGTGCTGC TTTTTGCTTG TTCCGTTCTG GCTGCTCCGG TCTGTGTTGT GGTTGTTTTG TTTCTTCTTG GGTGTGGGCC TTGCGGTTTT GGCTGTGGGC CCTTTGGGGC CTTGGCTTCT GGCTCCAT CCACATGATT GCTTAGATTT GTGCTGTATC TCTCAGGATT ATCACTGATT ACACATCCAA CCAGTGCCAG CCAAAAGGAT GCCCTGAGGC AAAGGGTTTC CATCTTGAGG CAAATTTGAG GACBTCCBC BTGBTTGCTT BGBTTTGTGC TGTBTCTCTC BGGBTTBTCB CTGBTTBCBC BTCCBBCCBG TGCCBGCCBB BBGGBTGCCC TGBGGCBBBG GGTTTCCBTC TTGBGGCBBB TTTGBGGB-3' **(FRAG. NO:1873) (SEQ. ID NO: 1886)**
5'-GBGGCBBBGGG-3' **(FRAG. NO:1874) (SEQ. ID NO: 1887)**
5'-GCCBGCCBB BBGGG-3' **(FRAG. NO:1875) (SEQ. ID NO: 1888)**
5'-CGCCTGGGCC C-3' **(FRAG. NO:1876) (SEQ. ID NO: 1889)**
5'-GTCTGTCCTCCCCGTCTCCTCCC-3' **(FRAG. NO:1339)(SEQ. ID NO:1348)**
5'-ACTGCTTCTCCCGGGGG-3' **(FRAG. NO:1340)(SEQ. ID NO:1349)**
5'-GCTTCCCCGGCTTC-3' **(FRAG. NO:1341)(SEQ. ID NO:1350)**
5'-GGGTGGCCGGTGTCCCGGGCTCCGGCGCGGCGGC-3' **(FRAG. NO:1342)(SEQ. ID NO:1351)**
5'-GGCTTCGGCTGC-3 **(FRAG. NO:1343)(SEQ. ID NO:1352)**
5'-GGGTGGGTGGCGCGG-3' **(FRAG. NO:1344)(SEQ. ID NO:1353)**
5'-GCTGCCGGGTCCGCGCGGCGCCTGGGCC-3' **(FRAG. NO:1345)(SEQ. ID NO:1354)**
5'-CTTGTGCTGCTTTT-3' **(FRAG. NO:1346(SEQ. ID NO:1355)**
5'-TGCTTGTTCCGTTC-3' **(FRAG. NO:1347)(SEQ. ID NO:1356)**
5'-TGGCTGCTCCGGTCTGTGTTGTGGTTGTTTTG-3' **(FRAG. NO:1348)(SEQ. ID NO:1357)**
5'-TTTCTTCTTGGGTGTGGG-3' **(FRAG. NO:1349)(SEQ. ID NO:1358)**
5'-CCTTGCGGTTTTGG-3' **(FRAG. NO:1350)(SEQ. ID NO:1359)**
5'-CTGTGGGCCCTTTG-3' **(FRAG. NO:1351)(SEQ. ID NO:1360)**
5'-GGGCCTTGGCTTCTGGCTC-3' **(FRAG. NO:1352)(SEQ. ID NO:1361)**
5'-CATCCACATG ATTGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC CAACCAGTGC CAGCCAAAAG GATGCCCTGA GGCAAAGGGT TTCCATCTTG AGGCAAATTT GAGGA-3' **(FRAG.NO:1353) (SEQ.ID NO:1362)**
5'-CBTCCBCBTG BTTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC CBBCCBGTGC CBGCCBBBBG GBTGCCCTGB GGCBBBGGGT TTCCBTCTTG BGGCBBBTTT GBGGB-3' **(FRAG. NO:1354)(SEQ. ID NO:1363)**

Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCCACCATGG AAACCCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA
ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT
CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT
TGCCCACAGC AGACTAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA
TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC
CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA
TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC CCTTTTTGCA
GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTTG ACAGGTACAG AGCAGTTGCC
TCCTGGAGTC GTGTTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC
TGTCCTTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA
GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG
CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA
TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC
AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTTCCCTC TTCATTTAAG CCGTATATTG
AAGAAAACTG TGTATAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT
ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA
ATTTAAAAAT TGTTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC
CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC
ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT GAATTCGGGA AAAAGTGAAG GTGTAAAAGC
AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC
TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC
ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA
TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC
AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA
GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA
CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT
CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG
TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT
TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT
GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG
CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT
GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC
TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG
TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT
GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC
ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT
GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA
GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA
CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC
GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG
CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA
TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC
AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT
GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT
AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG
TGCCAGTATC CCGAATTC GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA
TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG
ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT
TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG
GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT
ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA
TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG
ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT
TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT
AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG
CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT
GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG
TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA
TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA
ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG

TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT
TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC
CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC
CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA
ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG
TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC
TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC
CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC
ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT
TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC
TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC
AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' **(FRAG. NO:___) (SEQ ID NO: 3014)**

5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC
AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC
CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT
TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC
TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG
GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
CTGGTGGCTC TTCCGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT
TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG
AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC
ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT
CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT
GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC
AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT
CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' **(FRAG. NO:___) (SEQ ID NO: 2482)**

5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC
AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC
CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT
TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC
TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG
GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
CTGGTGGCTC TTCCGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT
TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG
AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC
ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT

CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3'**(FRAG. NO:__) (SEQ ID NO: 2470)**

5'-GCCACCATGG AAACCCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT TGCCCACAGC AGACTAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTCGGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC CCTTTTTGCA GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTTG ACAGGTACAG AGCAGTTGCC TCCTGGAGTC GTGTTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCCTTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTTCCCTC TTCATTTAAG CCGTATATTG AAGAAAACTG TGTATAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA ATTTAAAAAT TGTTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT-3' **(FRAG. NO:_) (SEQ ID NO: 2469)**

Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments

5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG BTCTGGTCGCT GTCGTBCCBG TCGGBCCBGT BBTTCBGBTC BTCBTTGGCT CCTBTTTCTT CTGCBBBCBG CTGBGTGGBG BCBBGBBBBB BGBCTGCCBB GGCCBCGBGG BTTTTCBTGT TGGBTTTTGC GBCGGBCBGT CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGCBC GTGGTCGCTC CGCGTTTCTC TGGTTCCTCC GGTCCCGCGG GGTGCTGTCT GGTCGCTGTC GTGGCTTGGG TCTCCGGGCG GTTTCCTTCC TTTTCCGC-3' **(FRAG. NO:1877) (SEQ ID NO: 1890)**

5'-CTCC GGGCGB-3' **(FRAG. NO:1878) (SEQ ID NO: 1891)**

5'-GGCCBCGBGG-3' **(FRAG. NO:1879) (SEQ ID NO: 1892)**

5'-GGGTCTCCGGGCG 3' **(FRAG. NO:1880) (SEQ ID NO: 1893)**

5'-GGG TCTCCGGGCG G-3' **(FRAG. NO:1881) (SEQ ID NO:1894)**

5'-CGTGGTCGCTCCGC-3' **(FRAG. NO:1355)(SEQ. ID NO:1364)**

5'-GTTTCTCTGGTTCCTCCG-3' **(FRAG. NO:1356)(SEQ. ID NO:1365)**

5'-GTCCCGCGGGGTGCTG-3' **(FRAG. NO:1357)(SEQ. ID NO:1366)**

5'-TCTGGTCGCTGTCGT-3' **(FRAG. NO:1358)(SEQ. ID NO:1367)**

5'-GGCTTGGGTCTCCGGGCG-3' **(FRAG. NO:1359)(SEQ. ID NO:1368)**

5'-GTTTCCTTCCTTTTCCGC-3' **(FRAG. NO:1360)(SEQ. ID NO:1369)**

5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG BTCTGGTCGCT GTCGTBCCBG TCGGBCCBGT BBTTCBGBTC BTCBTTGGCT CCTBTTTCTT CTGCBBBCBG CTGBGTGGBG BCBBGBBBBB BGBCTGCCBB GGCCBCGBGG BTTTTCBTGT TGGBTTTTGC GBCGGBCBGT CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGCB-3' **(FRAG. NO:1882) (SEQ ID NO: 1895)**

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG TGTBGGCBGC TGCCCBBBGG BCBBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCCG BGGTGTTBGT GGBGBTGTTT GGGGBGBGGT CTGGGTCCBC CGGGBGGBCG TTBTCCBTTT CGBBGCTBGG CGGTBBBGCC CTBCTBTCTG TBCBCBBCCC CCCTCTGCBG CBGBGTCCTG TCGTGGCGCC TGGGGCTCBG GGTCCGGGC TAAGATGATC CACATCACTA CCACGTTGCC CACCACAGAG GTCACCACAA TGACCGTGTA GGCAGCTGCC CAAAGGACAA TTTGCCAGGC TGGTTGCACG AACTGATTGG GTTCCGAGGT GTTAGTGGAG ATGTTTGGGG AGAGGTCTGA GTCCACCGGG AGGACGTTAT CCATTTCGAA GCTAGGCGGT AAAGCCCTAC TATCTGTACA CAACCCCCCT CTGCAGCAGA GTCCTGTCGT GGCGCCTGGG GCTCAGGGTC CGTCCTGTCG TGGCGCCTGG GGCTCTTCTT TTGTGGGCTC TTTCGTGGCT GTGGCTGTGG TCTCTGTGGT TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG GGGCCGTCCT CTGGCTCCTC CTCGTGGGCC CCC-3' **(FRAG. NO:1883) (SEQ. ID NO:1896)**

5'-GGGBGGBCG-3' **(FRAG. NO:1884) (SEQ. ID NO:1897)**

5'-GGGTC CG-3' **(FRAG. NO:1885) (SEQ. ID NO:1898)**

5-'GGGCC CCC-3' **(FRAG. NO:1886) (SEQ. ID NO:1899)**

5'-GTCCTGTCGTGGCGCCTGGGGCTC-3' **(FRAG. NO:1361)(SEQ. ID NO:1370)**

5'-TTCTTTTGTGGGCT-3' **(FRAG. NO:1362)(SEQ. ID NO:1371)**
5'-CTTTGGTGGCTGTGGCTG-3' **(FRAG. NO:1363)(SEQ. ID NO:1372)**
5'-TGGTCTCTGTGGTTG-3' **(FRAG. NO:1364)(SEQ. ID NO:1373)**
5'-CTGCCCTGGGTCTGG-3' **(FRAG. NO:1365)(SEQ. ID NO:1374)**
5'-GGGTGTGGCCTTGGGGCCGTCCTCTGGCTCCTCCTCGTGGGCCCCC **(FRAG.NO:1366)(SEQ.ID NO:1375)**
5'-GGGCTAAGAT GATCCACATC ACTACCACGT TGCCCACCAC AGAGGTCACC ACAATGACCG TGTAGGCAGC
TGCCCAAAGG ACAATTTGCC AGGCTGGTTG CACGAACTGA TTGGGTTCCG AGGTGTTAGT GGAGATGTTT
GGGGAGAGGT CTGAGTCCAC CGGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGTA
CACAACCCCC CTCTCCAGCA GAGTCCTGTC GTGGCGCCTG GGGCTCAGGGTCC-3' **(FRAG.NO:1367)(SEQ.ID NO:1376)**
5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG TGTBGGCBGC
TGCCCBBBGG BCBBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCCG BGGTGTTBGT GGBGBTGTTT
GGGGBGBGGTC TGBGTCCBCC GGGBGGBCGT TBTCCBTTTC GBBGCTBGGC GGTBBBGCCC TBCTBTCTGTB
CBCBBCCCCC CTCTGCBGCB GBGTCCTGTC GTGGCGCCTG GGGCTCBGGG TCC-3' **(FRAG. NO:1368) (SEQ. ID NO:1377)**

<u>Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments</u>

5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG
BBBGBGCBGC BGGGGGBGBG GBBGBBGCBG CBTCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTC
CTTTCCBGTC TTGCGTTTTB TBBCTCCCBG BBGGCBBGBG BGGGGCBBGG CGTTTTCTTC TCTCGCTGGT
TTTCCTTTCC TGGCAGTGGG TGGGGGTGGG GGTGGGGTGG CTTCCTTGTT CCTGGGGGTG TCCTCTTGCT
CTGGGCTTTT CTCCCCTTTT CCTTCCTGTC TGTTTTCCTG GGGCTCTCCT CTGTCTCTGT GTCCTTGCCC
TGGCCCTCTT CCCTCTCCTG TCTCCTGTCC CTGTGTTCCG CCCGTCTTCC
CTCTCCTGAC CTCCTTTTCC TCCGCTGGGT GGGGCCCTGC CTGTTCTCTG CTCCCTGGCT TGGGGTTTCT
TCTGTGTGTC TTCTTCCTCT GTTGGCTGGC TTTCTCCTTC TTTTGTCTTC CTGGGTGCCC CTTCTTCCTT
TCTTGGGTCC TTGGTGCTTG GGCTGGG TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA
TCTCTCCATG TCCACTCCCC CTGTATCTTG CCATTCTTGA CCTGCATTTC CATCCTCCTT ACCTTCCCTA
GAGGCCAACT CATTTTCTTT GAAAAACCTG GCATTTCCCA GAAAAAAAAG TGAAGGGCTG GGAGCTGTCC
GTTGTCCTGA TTTGCTCCCT CTGCCCTTGC TTCCAAATGT GGTTGGAAAG AAGCACTATT GAAAAATCCC
TAAACGCACC CCTGCAGGGT TGGCTCTACC CTGTAGCCAT GGACACATGC TGTTGATACC ACCTGCCTCA
TGAGTCTCAC ATAATTTGCC CTTTCACACT ATCTACCCCA TCAGCCTTAC CAAAACCATA CCTGCATCCT
GGGCAGCATC TGCCCTTCAA GAGACTAAGG AATCTCCTTG CAACCAAGAA TGACTAGACC AATGAGACAC
CCTTTAAGGC CCCAGCACAA TATAGAAATC CCACAATATG GTAATCCCAG TAAGGAGCTA TCAAGCCATT
GCAGGACCAT CTAGAATACA ACTAGAGTAT AGTTCCTTTC AATCCAGGAA CTATACTCTA ACAGCTTGGC
TCACAGGAAC CAGAAGTGAA GATGATGAGG ATCAGGGCTG AGCCTGTGAG CACCAGCTCC ACCACTGACA
CCAACCACAG ATTAAACAAG CATCTTGTGG ACCCCTGGGA TGGAAAGAAT AGTTGTTGCC TTATCAACCT
CCCCCACAGC CCACACAGAA AAGATAAAAT CATCATGGCT ACAGTGTTAC AGAAGATGAT GACCCAAGGA
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AACACTGGGA TAATCTCCAA GGATCTCTCC ATATCTCATT CTCCTGGATA CACTGTCCAC TCAGAAATAT
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AGGCAAATTA A-3' **(FRAG. NO:1887) (SEQ. ID NO:3015)**

5'-ATCATCGGGG GCACAGAATC CAAGCCACAT TCCCGCCCCT ACATGGCCTA CCTGGAAATT GTAACTTCCA
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5'-TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA TCTCTCCATG TCCACTCCCC CTGTATCTTG
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GCTGCTCTTT CTCTTGTGCT CCAGAGCTGA AGCTGGTGAG TATCAGGGTT CTTCCCTCTG AAATCTGCAG
TATCAGCTCC TGAAACAAAG ATGTTTAGTC TGAAATAGCT GACTCCTAAA CAGGGTTCCA AGATCTCTCT
TCAAGAGTCC CACAGAGGAA ATTTCCACTT GGGATGTGTG CCACCCCACC CCCACCCCCA CCCACTGCCA
TTCTCTACAG CCTAGGACAC CCCCAGGAAC AAGGAATTTC ACCTCAATTG TAGAAAAGCC CAGAGCAAGT
GGAAGGAAAA GGGGTATCCC CAGGAAAACA GACATGTCCT CTTAATCTTC TGAGCATCAG GGCTACCCAT
TACTTTGTGA CTTTCTCACT CTGTGACCAT GCTCAAGAGC TATGGAGAAA TCTAAAACAG GAACCTGGAC
AGTGGGTCCT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC AAGGTGGGAG TGGGAGAAGT CTGAGATGAA
AACATCAGAA TGGAGCAGAG GCAAGAATGA GATTTCACCT GGGAGGTTAT GGGTGGGGAA AGATACGAAA
TACAGGAGAC AGGAGAGGGA AGATGGGCGG AACACAGGGT GAGAATGAGA TTCCAGGGAA GCCTAGCTCA
GCTTTAACCC AATTTGTCCA TTCATTGGAG AGAGTATCTA TGGCCGTGTT CAAACCCTGG GGTGCTCTGT
TCCAGGGGAG ATCATCGGGG GCACAGAATG CAAGCCACAT TCCCGCCCCT ACATGGCCTA CCTGGAAATT
GTAACTTCCA ACGGTCCCTC AAAATTTTGT GGTGGTTTCC TTATAAGACG GAACTTTGTG CTGACGGCTG
CTCATTGTGC AGGAAGGTGA GACAACAGGG TCTATTTATC TCCAAATGGG AGATGAACAA CCAGAGTAGC
ATCCAGGAAT ACACCTGCAC TGGGGACTGA AGAGGGGGTC CTGGGTCTTG TCAACTTTCA GGAGAGGGAA

GACTTTGGGC TGAAAGACTT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC
CTTCGGAGGA AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCCTCACC CCTACCCAAC
TCAAGACACA CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CCTTTTCAAG
AACACTGGCT CTACTTCTCA GGGTCCTGAA CCCATCATTT TATGGGAGCA GAGAACAGGT CTACATAAGA
CCCCCACTTT CCCCTTTTAA CTGATATCTC CTGCTTCAGG GGCTGGCCCT CATGCAGGGT TCCCTGAATT
AGGAAGTGTG AACCCTGTCC CCTGAGTCCT CCCTGGCCTG TTCAGTCCCC AGCAATTCCA GGGGTCGTAG
AAATTGTGTC TGTTTCCTGA GAAAGCTCTT TCATGAGTTA AGCCTGAGCC CTCAAATGCC ACAAGTGGCC
CATGAAAAGG GAGATGGGTA GAGTCCGGCN ACCCAGTGAC AGAGTTTAGT CCTCTTTTCT CAGAATGAGC
TCACCTCAGA AGAAACCCCA AGCCATCACT GTCGCCTCCT TTTCCTTCCT TCTTCCTCAC AGCAGGTCTA
TAACAGTCAC CCTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTTATAAA
GCAATTCCGT CATCCAAAAT ATAACACTTC TACTCTTCAC CACGATATCA TGTTACTAAA GGTGACAACA
CCTCTCTTCT CCCTTTCCAC TTCCCATTCT CCTAAGCTTC TCCTTCAGGT CCTCATTGCC CTGAATTTTT
CTTAGGACTT GGCTATAACA TGAAGCTACT CACCCTGTCC CTCCCTGATC ACCTCCAACT GTCCAGAGCC
CATTTCGAGG ACTCACAGTC CTTCATTCCC TTCACAGTTG AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG
GGGACACTCC CCTTCCCATC ACAATTCAAC TTTGTCCCAC CTGGGAGAAT GTGCCGGGTG GCTGGCTGGG
GAAGAACAGG TGTGTTGAAG CCGGGCTCAG ACACTCTGCA AGAGGTGAAG CTGAGACTCA TGGATCCCCA
GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCCAG GAAGACAAAA
TCTGCATTTA AGGTGATCCT CCAACTAGGT TTCCTCTCCA AAACTCACTG TTCAGGGACC TGAATGCTCT
TAGAAGGAGA TGGGGTCAGC AGGTTGTCAG TCAGGTGACA GGGTGAGCAT CACAGGAATT GCTGTCCTCC
CGTGGTCCAA GACAGCCTCT GACCATCCAT TCCAGTCTAC TGCACTGGGG GCATGGGGTG ACTGTGGAGA
ATGTGGATGA CGGTCCCAAG AAAGGAAGAA GGGGCATCAG AACTAGATGT ATAAGTGAGG AGCTCCACCT
CCTGGGTCTG ACTTTAGGTC TCACTGTGAC TCCAAGCTGG CTGGCAGACA GGAGTGGAGG ACTTCCCGGG
CTCACCTTCT TCTCTCTCTC CTCCCCCTAC AGGGAGACTC TGGGGGCCCT CTTCTGTGTG CTGGGGTGGC
CCAGGGCATC GTATCCTATG GACGGTCGGA TGCAAAGCCC CCTGCTGTCT TCACCCGAAT CTCCCATTAC
CGGCCCTGGA TCAACCAGAT CCTGCAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGGAAGCTGG
AACTGGACCT TAGCAGCAAA GTGTGTGCAA CTCATTCTGG TTCTACCCTT GGTTCCCTCA GCCACAACCC
TAAGCCTCCA AGAGGTCTCC TACAGGTAAC AGAACTTTCA ATAAACTTCA GTGAAGACAC AGCTTCTAGT
CGTGAGTGTG TGTCCCTCTC TGCTGCTCTC TTCTCCTGCA CATGTGACCT GATTCCCAGC CCAAGCACCA AGGA-3'
(FRAG. NO:) (SEQ. ID NO:2467)

5'-GGBGCBCBBG-3' **(FRAG. NO:1888) (SEQ. ID NO:1901)**
5'-GBBGCBGC-3' **(FRAG. NO:1889) (SEQ. ID NO:1902)**
5'-GGGGCBBGG CG-3' **(FRAG. NO:1890) (SEQ. ID NO:1903)**
5'-CGTTTTCTTCTCTC-3' **(FRAG. NO:1369)(SEQ. ID NO:1378)**
5'-GCTGGTTTTCCTTTCC-3' **(FRAG. NO:1370)(SEQ. ID NO:1379)**
5'-TGGCAGTGGGTGGGGGTGGGGGTGGGGTGGC-3' **(FRAG. NO:1371)(SEQ. ID NO:1380)**
5'-TTCCTTGTTCCTGGGGGTGTCCT-3' **(FRAG. NO:1372)(SEQ. ID NO:1381)**
5'-CTTGCTCTGGGCTTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1382)
5'-CCCCTTTTCCTTCC-3' (FRAG. NO:1374)(SEQ. ID NO:1383) [
5'-TGTCTGTTTTCCTGGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1384)
5'-CTCTCCTCTGTCTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1385)
5'-CCTTGCCCTGGCCC-3' (FRAG. NO:1377)(SEQ. ID NO:1386)
5'-TCTTCCCTCTCCTGTCTCCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1387)
5'-CCCTGTGTTCCGCCC-3' (FRAG. NO:1379)(SEQ. ID NO:1388)
5'-GTCTTCCCTCTCCTG-3' (FRAG. NO:1380)(SEQ. ID NO:1389)
5'-ACCTCCTTTTCCTCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1390)
5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1391)
5'-CCTGTTCTCTGCTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1392)
5'-TGGCTTGGGGTTTCTTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1393)
5'-TGTGTCTTCTTCCTCTGTT-3' (FRAG. NO:1385)(SEQ. ID NO:1394)
5'-GGCTGGCTTTCTCCTTC-3' (FRAG. NO:1386)(SEQ. ID NO:1395)
5'-TTTTGTCTTCCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1396) [1397)]
5'-TGCCCCTTCTTCCTTTCTTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1397)
5'-TCCTTGGTGCTTGCGCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1398)
5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG
BBBGBGCBGC BGGGGGBGBG GBBGBBGCBG CBTCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTC
CTTTCCBGTC TTGGGTTTTB TBBCTCCCBG BBGGCBBGBG BGGGGCBBGG-3' **(FRAG.NO:1891) (SEQ.ID NO:1904)**

__Endothelial Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments__

5'-GCGTCTTGGG GTGCBGGGCC CBTCCTGCTG CGCCTGGGCG CTGCTGTGCG TCCGTCTGCT GGGGGGCCGG
GGTGGCTGGG CCCTGCTTGC CGCACGACCC CGGGCCGACC CGAGGCTCGG GGGGCTGTGT TCTGGCGCTG
GTGGGCTTGG GCCCCTCTGG GGGCTGGGTT TCCTGCTGCG CCTGGGCGCT GGCGTCTTGG GGTGCGGGGC
CGGGGGGCCG GGGGGCCGCT GTTCGTGGGC CTGGGGGTGC CTGTGGCTGC CGGTTGCCCC GGTTGGTGGC

GCCGTCCTGC TGCCGGTCGT TGGCTGGGTC CCCCCGCCCG TTTCCTGGGG TCCGCGTGGG GTGCTCCGGT TCCTCGTGCC GCTGCTGCCT TGTCTTTCCG GCCGTGGCGG CGTGGTGGTC CGCCCCCCCT GGCCTTCTGC TCGGGGTCTG GCTCGTTGCC GGTGCCCTTG GCGGCGGTCT TCTTCCTGGT GGCTCTGGGC CCGGCCGGTC TCGGGCGTCT CGTCTTCGCT CTTGTGCTGT TCCGGCCGCT CCTTCCTCTT CCGCCGCCGC CGCTCCCCGC CCGCTCGTCG CCCTGGCCCG GCCTCCTCCT GGCCGCTGTC TCGGGCGGCG GCCTTGGCGC TCCGTTTGGG GCTGCCTCTG GCGCTTCCGG CCCTCGGCCT GGGCGCTCTC TTCCGCCTGT GCTGGTGGCC CTCGTGGGCC CCTCCTGGCC TCCGGTGTCC TGTGGTCCCC CGGCTGGTGG CCGGGCCGGT TGGGCGGGCG TGGGCGCCGG CGGGTCCTCC GGGCTGCCCT TCTCCGCCGG GGGTCCCGCG CTCCTGCTGT TCCCTGGGCT CTTCTGCCTC TCTCCTGGGT GGGTGCTGGG TGCCGGGGTC TCCGGGCTTG CCCCGCGCTG CTGGGCGTTC TGCGGTCTTG GGGTTGTCTG TGGCCCCGCT CGTGTCGCCC TCCGTCGCCC GTCGCCGGCC TCGTCCCCTC CTGGGTGCGC GGCGGGCTGG TCCTGGCGTT TTGCTCCTTC CTGGGCGTCT TGGGGTGCBG GGCCCBTCCT GCTGCGCCTG GGCGCTGCTG TGCCTCCGTC TGCTGGGGGG CCGGGGTGGC TGGGCCCTGC TTGCCGCACG ACCCCGGGCC GACCCGAGGC TCGGGGGGCT GTGTTCTGGC GCTGGTGGGC TTGGGCCCCT CTGGGGGCTG GGTTTCCTGC TGCGCCTGGG CGCTGGCGTC TTGGGGTGCG GGGCCGGGGG GCCGGGGGGC CGCTGTTCGT GGGCCTGGGG GTGCCTGTGG CTGCCGGTTG CCCCGGTTGG TGGCGCCGTC CTGCTGCCGG TCGTTGGCTG GGTCCCCCCG CCCGTTTCCT GGGCTCCGCG TGGGGTGCTC CGGTTCCTCG TGCCGCTGCT GCCTTGTCTT TCCGGCCGTG GCGGCGTGGT GGTCCGCCCC CCCTGGCCTT CTGCTCGGGG TCTGGCTGGT TGCCGGTGCC CTTGGCGGCG GTCTTCTTCC TGGTGGCTCT GGGCCCGGCC GGTCTCGGGC GTCTCGTGTT CGCTCTTGTG CTGTTCCGGC CGCTCCTTCC TCTTCCGCCG CCGCCGCTCC CCGCCCGCTC GTCGCCCTGG CCCGGCCTCC TCCTGGCCGC TGTCTCGGGC GGCGGCCTTG GCGCTCCGTT TGGGGCTGCC TCTGGCGCTT CCGGCCCTCG GCCTGGGCGC TCTCTTCCGC CTGTGCTGGT GGCCCTCGTG GGCCCCTCCT GGCCTCCGGT GTCCTGTGGT CCCCCGGCTG GTGGCCGGGC CGGTTGGGCG GGCGTGGGCG CCGGCGGGTC CTCCGGGCTG CCCTTCTCCG CCGGGGGTCC CGCGCTCCTG CTGTTCCCTG GGCTCTTCTG CCTCTCTCCT GGGTGGGTGC TGGGTGCCGG GGTCTCCGGG CTTGCCCCGC GCTCCTGGGC GTTCTGCGGT CTTGGGGTTG TCTGTGGCCC CGCTCGTGTC GCCCTCCGTC GCCCGTCGCC GGCCTCGTCC CCTCCTGGGT GCGCGGCGGG CTGGTCCTGG CGTTTTGCTC CTTCCTGG-3' **(FRAG. NO:1892) (SEQ. ID NO 1905)**

5'-GCGGGGCCG-3' **(FRAG. NO:1893) (SEQ. ID NO: 1906)**

5'-CGGGGGGC-3' **(FRAG. NO:1894) (SEQ. ID NO: 1907)**

5'-GCGCGGCGGGC-3' **(FRAG. NO:1895) (SEQ. ID NO: 1908)**

5'-CTGTGCGTCCGTCTGCTGG **(FRAG. NO:1390)(SEQ. ID NO:1399)**

GGGGCCGGGGTGGCTGGGCCCTGCTTGCCGC (FRAG. NO:1391)(SEQ. ID NO:1400)

ACGACCCCGGGCCGACCCGAG (FRAG. NO:1392)(SEQ. ID NO:1401)

GCTCGGGGGGCTGTGTTCTGGCGCTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1402)

CTTGGGCCCCTCTGGGGGCTGGGTT (FRAG. NO:1394)(SEQ. ID NO:1403)

TCCTGCTGCGCCTGGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1404)

GCGTCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1405)

GGGGCCGGGGGGCCGGGG (FRAG. NO:1397)(SEQ. ID NO:1406)

GCCGCTGTTCGTGGGCCTGGG (FRAG. NO:1398)(SEQ. ID NO:1407)

GGTGCCTGTGGCTGCC (FRAG. NO:1399)(SEQ. ID NO:1408)

GGTTGCCCCGGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1409)

GCCGTCCTGCTGCCGGT (FRAG. NO:1401)(SEQ. ID NO:1410)

CGTTGGCTGGGTCCCCCCGC (FRAG. NO:1402)(SEQ. ID NO:1411)

CCGTTTCCTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1412)

GCGTGGGGTGCTCC (FRAG. NO:1404)(SEQ. ID NO:1413)

GGTTCCTCGTGCCG (FRAG. NO:1405)(SEQ. ID NO:1414)

CTGCTGCCTTGTCTTTCC (FRAG. NO:1406)(SEQ. ID NO:1415)

GGCCGTGGCGGCGTGGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1416)

GCCCCCCCTGGCCTTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1417)

GGGGTCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1418)

TGCCGGTGCCCTTGGCGGC (FRAG. NO:1410)(SEQ. ID NO:1419)

GGTCTTCTTCCTGGTG (FRAG. NO:1411)(SEQ. ID NO:1420)

GCTCTGGGCCCGGCCGGTCTCGG (FRAG. NO:1412)(SEQ. ID NO:1421)

GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1422)

CTCTTGTGCTGTTCCGGCCG (FRAG. NO:1414)(SEQ. ID NO:1423)

CTCCTTCCTCTTCCGCCGCC (FRAG. NO:1415)(SEQ. ID NO:1424)

GCCGCTCCCCGCCC (FRAG. NO:1416)(SEQ. ID NO:1425)

GCTCGTCGCCCTGGCCC (FRAG. NO:1417)(SEQ. ID NO:1426)

GGCCTCCTCCTGGCCGC (FRAG. NO:1418)(SEQ. ID NO:1427)

TGTCTCGGGCGGCGGCCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1428)

GCTCCGTTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1429)

CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1430)

GGCCCTCGGCCTGGGCGCTC (FRAG. NO:1422)(SEQ. ID NO:1431)

TCTTCCGCCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1432)
TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1433)
GCCCCTCCTGGCCTCCGGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1434)
TGTGGTCCCCCGGCTGGT (FRAG. NO:1426)(SEQ. ID NO:1435)
GGCCGGGCCGGTTGGGCGGGC (FRAG. NO:1427)(SEQ. ID NO:1436)
GTGGGCGCCGGCGGGTCCTCC (FRAG. NO:1428)(SEQ. ID NO:1437)
GGGCTGCCCTTCTCC (FRAG. NO:1429)(SEQ. ID NO:1438)
GCCGGGGGTCCCGC (FRAG. NO:1430)(SEQ. ID NO:1439)
GCTCCTGCTGTTCCCTGGGCTCTTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1440)
TCTCTCCTGGGTGGGTGCTGGGTGCCG (FRAG. NO:1432)(SEQ. ID NO:1441)
GGGTCTCCGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1442)
CCCCGCGCTGCTGGGCGTTCTGC (FRAG. NO:1434)(SEQ. ID NO:1443)
GGTCTTGGGGTTGTC (FRAG. NO:1435)(SEQ. ID NO:1444)
TGTGGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1445)
TGTCGCCCTCCGTCGCC (FRAG. NO:1437)(SEQ. ID NO:1446)
CGTCGCCGGCCTCGTCC (FRAG. NO:1438)(SEQ. ID NO:1447)
CCTCCTGGGTGCGC (FRAG. NO:1439)(SEQ. ID NO:1448)
GGCGGGCTGGTCCT (FRAG. NO:1440)(SEQ. ID NO:1449)
GGCGTTTTGCTCCTTCCTGG (FRAG. NO:1441)(SEQ. ID NO:1450)
5'-GCGTCTTGGGGTGCBGGGCCCBTCCTGCTGCGCCTGGGCGCTG-3' **(FRAG. NO:1896) (SEQ. ID NO: 1909)**

Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTGCCCCBGT TTTTGBTCCT CBCBTGCCGT GGGGBGGBCB BTGGCTGCCT CCCCGGGGTT TCTGCTGCTT
GCTGCTTCTT TCCCGTCTCC CTTCTTTCCC GTCTCCTTTT TGCCTCTTTG GGTTCCTGTT GTTTCTGGCC
TGCTTGGTGG CGGCTTGTGC GTTTCCTCTC TCTTCTCTTG GGTCTCCGCT TCTCGTCCTG CCTTTTCCTG
TCTCTGTCGC GCCCTTCCTC CTCCGGCGTC CTCCTGCCCT GTGCTGTTTG CCTCGGGTGG TGCGGGTCCC
GGTGCTCCCC CGGCGGGCCG GCTGGTTGCC TGGGCCTGTC TGGTGGGGTG TGGGGCCGCT GGGTTGGGGG
TGTGGTGGGC TCTTCTGTGG CCTGTGGGGC TGTTGGTGTC TCTGTGGGCG TGTGCTGGGT CTTGGGGCTT
CCTCCCTTGT GCTGGGTGCG GCCTCCCCGC CCCCCTTCTG GGCCGGTGGC CTGGCTCCTT GTGGGCGCTT
CTGGCTCTTG CCCTGTCCTT CTTCGCCTCG TGGCTGCTGG GCTGC CATATGTATG GGAATACTGT ATTTCAGGCA
TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC CCTTGTAATC CTAGCACTTT GAGAGGCTGA
AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC AGTCTCTACC
AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC TGTAGTCCCA GCTACTCAGG AGGCTGAGGT
GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCCAGTCTT
GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA ATAAATAAAA TAAATGAAAT GAAATTATAA
GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCCAT TATAAGGGAA GGAATTTAAT CCTACCTGCC
ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT AGTAAGACCA ACATCTCAGA GGCCTCTCTG
TGCCAATAGC CTTCCTTCCT TTCCCTTCCA AAAACCTCAA GTGACTAGTT CAGAGGCCTG TCTGGAATAA
TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGTG TGTTCCATAC TGTCAATATT
CCCCCAGCTT CCTGGACTCC TGTCACAAGC TGGAAAAGTG AGAGGATGGA CAGGGATTAA CCAGAGAGCT
CCCTGCTGAG GAAAAAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT TGGCCAAATA AAACCTGGCT
CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC TGCCACCTTG GACTTGGGAC CAGAAAGAGG
TGGGTTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG CAAGATCAGG TCACCCACAG GCCCTGGCAG
TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGGAC ACTCCCTTTG GAAACCAAAA AAAAAAAAAA
AAAAAAGAGA CCTTTATGCA AAAACAACTC TCTGGATGGC ATGGGGTGAG TATAAATACT TCTTGGCTGC
CAGTGTGTTC ATAACTTTGT AGCGAGTCGA AAACTGAGGC TCCGGCCGCA GAGAACTCAG CCTCATTCCT
GCTTTAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG
CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA GGTGAGTTGC C
CATATGTATG GGAATACTGT ATTTCAGGCA TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC
CCTTGTAATC CTACCACTTT GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA
TGGACAACAT GGTGAAACCC AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC
TGTAGTCCCA GCTACTCAGG AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA
GCAGAGATCG TGCCACTCCG CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA
ATAAATAAAA TAAATGAAAT GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCCAT
TATAAGGGAA GGAATTTAAT CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT
AGTAAGACCA ACATCTCAGA GGCCTCTCTG TGCCAATAGC CTTCCTTCCT TTCCCTTCCA AAAACCTCAA
GTGACTAGTT CAGAGGCCTG TCTGGAATAA TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA
TTTTCCAGTG TGTTCCATAC TGTCAATATT CCCCCAGCTT CCTGGACTCC TGTCACAAGC TGGAAAAGTG
AGAGGATGGA CAGGGATTAA CCAGAGAGCT CCCTGCTGAG GAAAAAATCT CCCAGATGCT GAAAGTGAGG
CCATGTGGCT TGGCCAAATA AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC
TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG
CAAGATCAGG TCACCCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGGAC

ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA CCTTTATGCA AAAACAACTC TCTGGATGGC ATGGGGTGAG TATAAATACT TCTTGGCTGC CAGTGTGTTC ATAACTTTGT AGCGAGTCGA AAACTGAGGC TCCGGCCGCA GAGAACTCAG CCTCATTCCT GCTTTAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA GGTGAGTTGC C-3' **(FRAG. NO:_)(SEQ. ID NO: 3016)**

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CCAGGGTCCC CTGCACCACG GTGTCTGCAG CACATGGCTC AACAGCCTGA AGCCCCAAGA CCCAGTGCCC

TGCTTTGTGC GGAATGCCAG CGCCTTCCAC CTCCCCGAGG ATCCCTCCCA TCCTTGCATC CTCATCGGGC CTGGCACAGG CATCGTGCCC TTCCGCAGTT TCTGGCAGCA ACGGCTCCAT GACTCCCAGC ACAAGGGAGT GCGGGGAGGC CGCATGACCT TGGTGTTTGG GTGCCGCCGC CCAGATGAGG ACCACATCTA CCAGGAGGAG ATGCTGGAGA TGGCCCAGAA GGGGGTGCTG CATGCGGTGC ACACAGCCTA TTCCCGCCTG CCTGGCAAGC CCAAGGTCTA TGTTCAGGAC ATCCTGCGGC AGCAGCTGGC CAGCGAGGTG CTCCGTGTGC TCCACAAGGA GCCAGGCCAC CTCTATGTTT GCGGGGATGT GCGCATGGCC CGGGACGTGG CCCACACCCT GAAGCAGCTG GTGGCTGCCA AGCTGAAATT GAATGAGGAG CAGGTCGAGG ACTATTTCTT TCAGCTCAAG AGCCAGAAGC GCTATCACGA AGATATCTTC GGTGCTGTAT TTCCTTACGA GGCGAAGAAG GACAGGGTGG CGGTGCAGCC CAGCAGCCTG GAGATGTCAG CGCTCTGAGG GCCTACAGGA GGGGTTAAAG CTGCCGGCAC AGAACTTAAG GATGGAGCCA GCTCTGCATT ATCTGAGGTC ACAGGGCCTG GGGAGATGGA GGAAAGTGAT ATCCCCCAGC CTCAAGTCTT ATTTCCTCAA CGTTGCTCCC CATCAAGCCC TTTACTTGAC CTCCTAACAA GTAGCACCCT GGATTGATCG GAGCCTCCTC TCTCAAACTG GGGCCTCCCT GGTCCCTTGG AGACAAAATC TTAAATGCCA GGCCTGGCGA GTGGGTGAAA GATGGAACTT GCTGCTGAGT GCACCACTTC AAGTGACCAC CAGGAGGTGC TATCGCACCA CTGTGTATTT AACTGCCTTG TGTACAGTTA TTTATGCCTC TGTATTTAAA AAACTAACAC CCAGTCTGTT CCCCATGGCC ACTTGGGTCT TCCCTGTATG ATTCCTTGAT GGAGATATTT ACATGAATTG CATTTTACTT TAATC 3' **(FRAG. NO:_)(SEQ. ID NO:2507)**

5'-GAATTCCCAC TCTGCTGCCT GCTCCAGCAG ACGGACGCAC AGTAACATGG GCAACTTGAA GAGCGTGGCC CAGGAGCCTG GGCCACCCTG CGGCCTGGGG CTGGGGCTGG GCCTTGGGCT GTGCGGCAAG CAGGGCCCAG CCACCCCGGC CCCTGAGCCC AGCCGGGCCC CAGCATCCCT ACTCCCACCA GCGCCAGAAC ACAGCCCCCC GAGCTCCCCG CTAACCCAGC CCCCAGAGGG GCCCAAGTTC CCTCGTGTGA AGAACTGGGA GGTGGGGAGC ATCACCTATG ACACCCTCAG CGCCCAGGCG CAGCAGGATG GGCCCTGCAC CCCAAGACGC TGCCTGGGCT CCCTGGTATT TCCACGGAAA CTACAGGGCC GGCCCTCCCC CGGCCCCCCG GCCCCTGAGC AGCTGCTGAG TCAGGCCCGG GACTTCATCA ACCAGTACTA CAGCTCCATT AAGAGGAGCG GCTCCCAGGC CCACGAACAG CGGCTTCAAG AGGTGGAAGC CGAGGTGGCA GCCACAGGCA CCTACCAGCT TAGGGAGAGC GAGCTGGTGT TCGGGGCTAA GCACGCCTGG CGCAACGCTC CCCGCTGCGT GGGCCGGATC CAGTGGGGGA AGCTGCAGGT GTTCGATGCC CGGGACTGCA GGTCTGCACA GGAAATGTTC ACCTACATCT GCAACCACAT CAAGTATGCC ACCAACCGGG GCAACCTTCG CTCGGCCATC ACAGTGTTCC CGCAGCGCTG CCCTGGCCGA GGAGACTTCC GAATCTGGAA CAGCCAGCTG GTGCGCTACG CGGGCTACCG GCAGCAGGAC GGCTCTGTGC GGGGGGACCC AGCCAACGTG GAGATCACCG AGCTCTGCAT TCAGCACGGC TGGACCCCAG GAAACGGTCG CTTCGACGTG CTGCCCCTGC TGCTGCAGGC CCCAGATGAG CCCCCAGAAC TCTTCCTTCT GCCCCCCGAG CTGGTCCTTG AGGTGCCCCT GGAGCACCCC ACGCTGGAGT GGTTTGCAGC CCTGGGCCTG CGCTGGTACG CCCTCCCGGC AGTGTCCAAC ATGCTGCTGG AAATTGGGGG CCTGGAGTTC CCCGCAGCCC CCTTCAGTGG CTGGTACATG AGCACTGAGA TCGGCACGAG GAACCTGTGT GACCCTCACC GCTACAACAT CCTGGAGGAT GTGGCTGTCT GCATGGACCT GGATACCCGG ACCACCTCGT CCCTGTGGAA AGACAAGGCA GCAGTGGAAA TCAACGTGGC CGTGCTGCAC AGTTACCAGC TAGCCAAAGT CACCATCGTG GACCACCACG CCGCCACGGC CTCTTTCATG AAGCACCTGG AGAATGAGCA GAAGGCCAGG GGGGGCTGCC CTGCAGACTG GGCCTGGATC GTGCCCCCCA TCTCGGGCAG CCTCACTCCT GTTTTCCATC AGGAGATGGT CAACTATTTC CTGTCCCCGG CCTTCCGCTA CCAGCCAGAC CCCTGGAAGG GGAGTGCCGC CAAGGGCACC GGCATCACCA GGAAGAAGAC CTTTAAAGAA GTGGCCAACG CCGTGAAGAT CTCCGCCTCG CTCATGGGCA CGGTGATGGC GAAGCGAGTG AAGGCGACAA TCCTGTATGG CTCCGAGACC GGCCGGGCCC AGAGCTACGC ACAGCAGCTG GGGAGACTCT TCCGGAAGGC TTTTGATCCC CGGGTCCTGT GTATGGATGA GTATGACGTG GTGTCCCTCG AACACGAGAC GCTGGTGCTG GTGGTAACCA GCACATTTGG GAATGGGGAT CCCCCGGAGA ATGGAGAGAG CTTTGCAGCT GCCCTGATGG AGATGTCCGG CCCCTACAAC AGCTCCCCTC GGCCGGAACA GCACAAGAGT TATAAGATCC GCTTCAACAG CATCTCCTGC TCAGACCCAC TGGTGTCCTC TTGGCGGCGG AAGAGGAAGG AGTCCAGTAA CACAGACAGT GCAGGGGCCC TGGGCACCCT CAGGTTCTGT GTGTTCGGGC TCGGCTCCCG GGCATACCCC CACTTCTGCG CCTTTGCTCG TGCCCGTGGAC ACACGGCTGG AGGAACTGGG CGGGGAGCGG CTGCTGCAGC TGGGCCAGGG CGACGAGCTG TGCGGCCAGG AGGAGGCCTT CCGAGGCTGG GCCCAGGCTG CCTTCCAGGC CGCCTGTGAG ACCTTCTGTG TGGGAGAGGA TGCCAAGGCC GCCGCCCGAG ACATCTTCAG CCCCAAACGG AGCTGGAAGC GCCAGAGGTA CCGGCTGAGC GCCCAGGCCG AGGGCCTGCA GTTGCTGCCA GGTCTGATCC ACGTGCACAG GCGGAAGATG TTCCAGGCTA CAATCCGCTC AGTGGAAAAC CTGCAAAGCA GCAAGTCCAC GAGGGCCACC ATCCTGGTGC GCCTGGACAC CGGAGGCCAG GAGGGGCTGC AGTACCAGCC GGGGGACCAC ATAGGTGTCT GCCCGCCCAA CCGGCCCGGC CTTGTGGAGG CGCTGCTGAG CCGCGTGGAG GACCCGCCGG CGCCCACTGA GCCCGTGGCA GTAGAGCAGC TGGAGAAGGG CAGCCCTGGT GGCCCTCCCC CCGGCTGGGT GCGGGACCCC CGGCTGCCCC CGTGCACGCT GCGCCAGGCT CTCACCTTCT TCCTGGACAT CACCTCCCCA CCCAGCCCTC AGCTCTTGCG GCTGCTCAGC ACCTTGGCAG AAGAGCCCAG GGAACAGCAG GAGCTGGAGG CCCTCAGCCA GGATCCCCGA CGCTACGAGG AGTGGAAGTG GTTCCGCTGC CCCACGCTGC TGGAGGTGCT GGAGCAGTTC CCGTCGGTGG CGCTGCCTGC CCCACTGCTC CTCACCCAGC TGCCTCTGCT CCAGCCCCGG TACTACTCAG TCAGCTCGGC ACCCAGCACC CACCCAGGAG AGATCCACCT CACTGTAGCT GTGCTGGCAT ACAGGACTCA GGATGGGCTG GGCCCCCTGC ACTATGGAGT CTGCTCCACG TGGCTAAGCC AGCTCAAGCC CGGAGACCCT GTGCCCTGCT TCATCCGGGG GGCTCCCTCC TTCCGGCTGC CACCCGATCC CAGCTTGCCC TGCATCCTGG TGGGTCCAGG CACTGGCATT GCCCCCTTCC GGGGATTCTG GCAGGAGCGG CTGCATGACA TTGAGAGCAA AGGGCTGCAG CCCACTCCCA TGACTTTGGT GTTCGGCTGC CGATGCTCCC AACTTGACCA TCTCTACCGC

GACGAGGTGC AGAACGCCCA GCAGCGCGGG GTGTTTGGCC GAGTCCTCAC CGCCTTCTCC CGGGAACCTG ACAACCCCAA GACCTACGTG CAGGACATCC TGAGGACGGA GCTGGCTGCG GAGGTGCACC GCGTGCTGTG CCTCGAGCGG GGCCACATGT TTGTCTGCGG CGATGTTACC ATGGCAACCA ACGTCCTGCA GACCGTGCAG CGCATCCTGG CGACGGAGGG CGACATGGAG CTGGACGAGG CCGGCGACGT CATCGGCGTG CTGCGGGATC AGCAACGCTA CCACGAAGAC ATTTTCGGGC TCACGCTGCG CACCCAGGAG GTGACAAGCC GCATACGCAC CCAGAGCTTT TCCTTGCAGG AGCGTCAGTT GCGGGGCGCA GTGCCCTGGG CGTTCGACCC TCCCGGCTCA GACACCAACA GCCCCTGAGA GCCGCCTGGC TTTCCCTTCC AGTTCCGGGA GAGCGGCTGC CCGACTCAGG TCCGCCCGAC CAGGATCAGC CCCGCTCCTC CCCTCTTGAG GTGGTGCCTT CTCACATCTG TCCAGAGGCT GCAAGGATTC AGCATTATTC CTCCAGGAAG GAGCAAAACG CCTCTTTTCC CTCTCTAGGC CTGTTGCCTC GGGCCTGGGT CCGCCTTAAT CTGGAAGGCC CCTCCCAGCA GCGGTACCCC AGGGCCTACT GCCACCCGCT TCCTGTTTCT TAGTCCGAAT GTTAGATTCC TCTTGCCTCT CTCAGGAGTA TCTTACCTGT AAAGTCTAAT CTCTAAATCA AGTATTTATT ATTGAAGATT TACCATAAGG GACTGTGCCA GATGTTAGGA GAACTACTAA AGTGCCTACC CCAGCTC-3' (FRAG. NO:_) (SEQ. ID NO:2508)

5'-CCCCGGGG-3' **(FRAG. NO:1898) (SEQ. ID NO: 1911)**

5'-GGGGCCGCTGGG-3' **(FRAG. NO:1899) (SEQ. ID NO:1912)**

5'-GGGGGTGTGG-3' **(FRAG. NO:1900) (SEQ. ID NO: 1913)**

5'-CTGCCTCCCCGGGGT-3' **(FRAG. NO:1442)(SEQ. ID NO:1451)**

5'-TTCTGCTGCTTGCTG-3' **(FRAG. NO:1443)(SEQ. ID NO:1452)**

5'-CTTCTTTCCCGTCTCC-3' **(FRAG. NO:1444)(SEQ. ID NO:1453)**

5'-CTTCTTTCCCGTCTCC-3' **(FRAG. NO:1445)(SEQ. ID NO:1454)**

5'-TTTTTGCCTCTTTG-3' **(FRAG. NO:1446)(SEQ. ID NO:1455)**

5'-GGTTCCTGTTGTTTCT-3' **(FRAG. NO:1447)(SEQ. ID NO:1456)**

5'-GGCCTGCTTGGTGGCG-3' **(FRAG. NO:1448)(SEQ. ID NO:1457)**

5'-GCTTGTGCGTTTCC-3' **(FRAG. NO:1449)(SEQ. ID NO:1458)**

5'-TCTCTCTTCTCTTGGGTCTCCGCTTCTCGTCCTGCC-3' **(FRAG. NO:1450)(SEQ. ID NO:1459)**

5'-TTTTCCTGTCTCTGTCGC-3' **(FRAG. NO:1451)(SEQ. ID NO:1460)**

5'-GCCGTTCCTCCTCC-3' **(FRAG. NO:1452)(SEQ. ID NO:1461)**

5'-GGCGTCCTCCTGCCC-3' **(FRAG. NO:1453)(SEQ. ID NO:1462)**

5'-TGTGCTGTTTGCCTCGG-3' (FRAG. NO:1454)(SEQ. ID NO:1463)

5'-GTGGTGCGGGTCCC-3' (FRAG. NO:1455)(SEQ. ID NO:1464)

5'-GGTGCTCCCCCGGC-3' (FRAG. NO:1456)(SEQ. ID NO:1465)

5'-GGGCCGGCTGGTTGCCTGGGC-3' (FRAG. NO:1457)(SEQ. ID NO:1466)

5'-CTGTCTGGTGGGGTGTGGGGCC-3' (FRAG. NO:1458)(SEQ. ID NO:1467)

5'-GCTGGGTTGGGGTGTGGTG-3' (FRAG. NO:1459)(SEQ. ID NO:1468)

5'-GGCTCTTCTGTGGCC-3' (FRAG. NO:1460)(SEQ. ID NO:1469)

5'-TGTGGGGCTGTTGGTG-3' (FRAG. NO:1461)(SEQ. ID NO:1470)

5'-TCTCTGTGGGCGTGTG-3' (FRAG. NO:1462)(SEQ. ID NO:1471)

5'-CTGGGTCTTGGGGCTTC-3' (FRAG. NO:1463)(SEQ. ID NO:1472)

5'-CTCCCTTGTGCTGGG-3' (FRAG. NO:1464)(SEQ. ID NO:1473)

5'-TGCGGCCTCCCCGC-3' (FRAG. NO:1465)(SEQ. ID NO:1474)

5'-CCCCCTTCTGGGCC-3' (FRAG. NO:1466)(SEQ. ID NO:1475)

5'-GGTGGCCTGGCTCCTTGTGG-3' (FRAG. NO:1467)(SEQ. ID NO:1476)

5'-GCGCTTCTGGCTCTTG-3' (FRAG. NO:1468)(SEQ. ID NO:1477)

5'-CCCTGTCCTTCTTCGCCTCGT-3' (FRAG. NO:1469)(SEQ. ID NO:1478)

5'-GGCTGCTGGGCTGC-3' (FRAG. NO:1470)(SEQ. ID NO:1479)

5'-CTGCCCCBGTTTTTGBTCCTCBCBTGCCGTGGGGBGGBCBBTGG-3'**(FRAG. NO:1901) (SEQ. ID NO: 1914)**

NF-kB Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCGGTG CCTCCTCTTG GCTGGTCCCT CGTTGTCCTT GGGCCCCGC TCCCGCTGCT CGGCCTCCGT GTTCTTTGGC CTCTTGCTCC GCCTGCTGTC TTGTCCCGTC CCCTCCTCGC TTGCGTTTCC CTCTTCCTTG TCTTCCAGGC CTTCCTCCGC TTCCGCTGCT GGGGCCCGCG CCGGGGGGGC GCTCGGCTCC GCGGCTTCCT CCCCGGCTGG GGGGTCCTGG TCTCCGGGGC CTGCGGCTCG CGGGCTCGGG GCTGCGTGCG CCGCGCGCGG CGTCCGCGGT GGGTGGCGCT GTCCCGCCGT GGTGTGTCTC CGTTCTCGTC CTGCGCCGTC CTGGTCTGCC CGTGGGGTCC TGGGCGTGGT GGGGGGCGTC TGGTGCCTCG TCTGCCCCGT GGGGCTTCGG GCTCGGGGCT GTTCGTCCCC CCTGCCGCTC TGTGGCCTCC GGGGCTCCTC GTTTTCGCTG CTTCGGGTGT CCTTCTCGGC GTGTGGCCCC GGGTCCCGGC CCTGCTGGGC TGGGCGGGGT CGCTGCCCTG GGCTTCTGGC CCGTCTGGTT GTCTGTCGGT GCTTGTCTCG GGTTTCTGGC CTCTGTGCTG GGCGCTTCTC TGCCTCCTGC TCCGCCCTCC TGGTGGCTCG GCTGGGGGTG CCCGTGCGGG GGTGGGTGTG GGGTGTTTTC GGGGTCCTCC CCTTCCC-3' **(FRAG. NO:1902) (SEQ. ID NO:1915)**

5'-GGGCGGGGTCGC-3' **(FRAG. NO:1903) (SEQ. ID NO:1916)**

5'-GCGCCGTCC-3' **(FRAG. NO:1904) (SEQ. ID NO:1917)**

5'-GGGCGTGGTGG-3' **(FRAG. NO:1905) (SEQ. ID NO:1918)**
5'-GTTGGGCTTGGCCGGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1480)
5'-CTGCCCGGTGCCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1481)
5'-TCTTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1482)
5'-TGTCCTTGGGCCCC-3' (FRAG. NO:1474)(SEQ. ID NO:1483)
5'-GCTCCCGCTGCTCGGCCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1484)
5'-GTTCTTGGCCTCTTGCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1485)
5'-GCCTGCTGTCTTGTCC-3' (FRAG. NO:1477)(SEQ. ID NO:1486)
5'-CGTCCCCTCCTCGCTTGCGTTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1487)
5'-CCTCTTCCTTGTCTTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1488)
5'-GGCCTTCCTCCGCTTCCGCTGC-3' (FRAG. NO:1480)(SEQ. ID NO:1489)
5'-TGGGGCCCGCGCCGG-3' (FRAG. NO:1481)(SEQ. ID NO:1490)
5'-GGGGGCGCTCGGCTCCGCGGCTTCCTCCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1491)
5'-CTGGGGGGTCCTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1492)
5'-TCTCCGGGGCCTGCGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1493)
5'-GGGCTCGGGGCTGCGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1494)
5'-GCGCGCGGCGTCCGCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1495)
5'-GGTGGCGCTGTCCCGCC-3' (FRAG. NO:1487)(SEQ. ID NO:1496)
5'-GTGGTGTGTCTCCGTTCTCGTCCTGCGCCGTC-3' (FRAG. NO:1488)(SEQ. ID NO:1497)
5'-CTGGTCTGCCCGTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1498)
5'-GGTCCTGGGCGTGGTGG-3' (FRAG. NO:1490)(SEQ. ID NO:1499)
5'-GGGGCGTCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1500)
5'-CTCGTCTGCCCCGTG-3' (FRAG. NO:1492)(SEQ. ID NO:1501)
5'-GGGCTTCGGGCTCGG-3' (FRAG. NO:1493)(SEQ. ID NO:1502)
5'-GGCTGTTCGTCCCCCTGCCGCTCTGTGGCCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1503)
5'-GGGGCTCCTCGTTTTC-3' (FRAG. NO:1495)(SEQ. ID NO:1504)
5'-GCTGCTTCGGGTGTCCTTCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1505)
5'-GGCGTGTGGCCCCGG-3' (FRAG. NO:1497)(SEQ. ID NO:1506)
5'-GTCCCGGCCCTGCTGGGCTGGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1507)
5'-GCTGCCCTGGGCTTCTGGCCCGTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1508)
5'-GGTTGTCTGTCGGT-3' (FRAG. NO:1500)(SEQ. ID NO:1509)
5'-GCTTGTCTCGGGTTTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1510)
5'-CCTCTGTGCTGGGC-3' (FRAG. NO:1502)(SEQ. ID NO:1511)
5'-GCTTCTCTGCCTCCTGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1512)
5'-GCCCTCCTGGTGGCTC-3' (FRAG. NO:1504)(SEQ. ID NO:1513)
5'-GGCTGGGGGTGCCCGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1514)
5'-GGGGTGGGTGTGGGGTGTT-3' (FRAG. NO:1506)(SEQ. ID NO:1515)
5'-TTCGGGGTCCTCCCCTTCCC-3' (FRAG. NO:1507)(SEQ. ID NO:1516)
5'-CGGCCCTTCTCACTGGAGGCACCGGGCAGTCCTCCATGGGAGG-3' **(FRAG.NO:1906)(SEQ.ID NO:1919)**

<u>Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGA GTT TCA TCT TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' **(FRAG. ID:1907) (SEQ. ID NO:1920)**
5'-GGG GGA GTT-3' **(FRAG. ID:1908) (SEQ. ID NO:1921)**
5'-G CCC TGG GCC C-3' **(FRAG. ID:1909) (SEQ. ID NO:1922)**
5'-GTT TCA TCT TGG CTT TAT CC-3' **(FRAG. NO:1508) (SEQ. ID NO:1517)**
5'-TCT CCC CTT GTT CCT CCC C-3' **(FRAG. NO:1509)(SEQ. ID NO:1518)**
5'-TCT CCT GCT CTG GRG TCT CCT C-3' **(FRAG. NO:1510)(SEQ. ID NO:1519)**
5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1520)
5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1521)
5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1513)(SEQ. ID NO:1522)
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1523)
5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1524)
5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGA GTT TCA TCT TCG-3' **(FRAG. ID:1910) (SEQ. ID NO:1923)**
5'-GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' **(FRAG. ID:1911) (SEQ. ID NO:1924)**

Human Eosinophil Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1525)
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO: 1526)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1527)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO: 1528)
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO: 1529)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO: 1530)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO: 1531)
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO: 1532)
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO: 1533)
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO: 1534)
5'-GGG GGB GTT TCB-3' (FRAG. NO:1526)(SEQ. ID NO: 1535)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO: 1536)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO: 1537)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO: 1538)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO: 1539)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO: 1540)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO: 1541)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO: 1542)
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1534)(SEQ. ID NO: 1543)
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1535)(SEQ. ID NO: 1544)
5'-GG GGB GTT TCB T-3' (FRAG. NO:1536)(SEQ. ID NO: 1545)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO: 1546)
5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO: 1547)
5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO: 1548)
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO: 1549)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO: 1550)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO: 1551)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO: 1552)
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1544)(SEQ. ID NO: 1553)
5'-G GGB GTT TCB TC-3' (FRAG. NO:1545)(SEQ. ID NO: 1554)
5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO: 1555)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO: 1556)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO: 1557)
5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO: 1558)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO: 1559)
5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO: 1560)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO: 1561)
5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO: 1562)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO: 1563)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO: 1564)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO: 1565)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO: 1566)
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO: 1567)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO: 1568)
5'-GB GTT TCB TCT T 3' (FRAG. NO:1560)(SEQ. ID NO: 1569)
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO: 1570)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO: 1571)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1563)(SEQ. ID NO: 1572)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO: 1573)
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO: 1574)
5'-B GTT TCB TCT TGG-3' (FRAG. NO:1565)(SEQ. ID NO: 1575)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO: 1576)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO: 1577)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO: 1578)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO: 1579)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO: 1580)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO: 1581)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO: 1582)
5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO: 1583)
5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO: 1584)

5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO: 1585)
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1577)(SEQ. ID NO: 1586)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1578)(SEQ. ID NO: 1587)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1579)(SEQ. ID NO: 1588)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO: 1589)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO: 1590)
5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1591)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO: 1592)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO: 1593)
5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO: 1594)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO: 1595)
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1587)(SEQ. ID NO: 1596)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO: 1597)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO: 1598)
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1590)(SEQ. ID NO: 1599)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO: 1600)
5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO: 1601)
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO: 1602)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO: 1603)
5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO: 1604)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO: 1605)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO: 1606)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO: 1607)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO: 1608)
5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO: 1609)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1601)(SEQ. ID NO: 1610)
5'-TCB TCT TGG CTT 3' (FRAG. NO:1602)(SEQ. ID NO: 1611)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO: 1612)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO: 1613)
5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO: 1614)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO: 1615)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO: 1616)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO: 1617)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO: 1618)
5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO: 1619)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO: 1620)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO: 1621)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO: 1622)
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO: 1623)
5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO: 1624)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO: 1625)
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1617)(SEQ. ID NO: 1626)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO: 1627)
5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO: 1628)
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO: 1629)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO: 1630)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO: 1631)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO: 1632)
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO: 1633)
5'-B GTT TCB TCT TGG-3' (FRAG. NO:1625)(SEQ. ID NO: 1634)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO: 1635)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO: 1636)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO: 1637)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO: 1638)
5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO: 1639)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO: 1640)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO: 1641)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO: 1642)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO: 1643)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO: 1644)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO: 1645)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO: 1646)

5'-GB GTT TCB TCT T-3' (FRAG. NO:1638)(SEQ. ID NO: 1647)
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1639)(SEQ. ID NO: 1648)
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1640)(SEQ. ID NO: 1649)
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO: 1650)
5'-GGB GTT TCB TCT 3' (FRAG. NO:1642)(SEQ. ID NO: 1651)
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1643)(SEQ. ID NO: 1652)
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1644)(SEQ. ID NO: 1653)
5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO: 1654)
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO: 1655)
5'-GG GGB GTT TCB T-3' (FRAG. NO:1647)(SEQ. ID NO: 1656)
5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO: 1657)
5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO: 1658)
5'-TCT CCT GCT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO: 1659)
5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO:1660)
5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO: 1661)
5'-GTT TCG CTC TTG TTG CCC-3' -3' (FRAG. NO:1653)(SEQ. ID NO: 1661)
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO: 1663)
5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO:1925)
5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO: 1926)

BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CCGTGTTGTC BGTGGTGCTG CCCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC TTGTTTTCCG TTTCTCTTGC CGTCTGTGGT T-3' **(FRAG. NO:1914) (SEQ. ID NO: 1927)**
5'-CCCGTTTGBGGTBTGGC-3'**(FRAG. NO:1915) (SEQ. ID NO: 1928)**
5'-GCTCCBCCBBTTCCCTTTTCTCC-3'**(FRAG. NO:1916) (SEQ. ID NO: 1929)**
5'-TTGTTTTCCGTTTCTCTTG-3'**(FRAG. NO:1917) (SEQ. ID NO: 1930)**
5'-CCGTCTGTGGTT-3'**(FRAG. NO:1918) (SEQ. ID NO: 1931)**
5'-CCCGTTTGAGGTATGGC-3'**(FRAG. NO:1919) (SEQ. ID NO: 1932)**
5'-GCTCCBCCAATTCCCTTTTCTCC-3'**(FRAG. NO:1920) (SEQ. ID NO: 1933)**

C/EBPNucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments

5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCCC GGCC-3' **(FRAG. NO:1921) (SEQ. ID NO: 1934)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCCC GGC-3' **(FRAG. NO:1922) (SEQ. ID NO: 1935)**
5'-GGGCCCB GCCCCGCCGCCTTTTCTBGCCCCGG-3' **(FRAG. NO:1923) (SEQ. ID NO: 1936)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCCG-3' **(FRAG. NO:1924) (SEQ. ID NO: 1937)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCC-3' **(FRAG. NO:1925) (SEQ. ID NO: 1938)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCC-3' **(FRAG. NO:1926) (SEQ. ID NO: 1939)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCC-3' **(FRAG. NO:1927) (SEQ. ID NO: 1940)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGC-3' **(FRAG. NO:1928) (SEQ. ID NO: 1941)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTBG-3' **(FRAG. NO:1929) (SEQ. ID NO: 1942)**
5'-GGGCCCBGCCCCGCCGCCTTTTCTB-3' **(FRAG. NO:1930) (SEQ. ID NO: 1943)**
5'-GGGCCCBGCCCCGCCGCCTTTTCT-3' **(FRAG. NO:1931) (SEQ. ID NO:1942) 1944)**
5'-GGGCCCBGCCCCGCCGCCTTTTC-3' **(FRAG. NO:1932) (SEQ. ID NO: 1945)**
5'-GGGCCCBGCCCCGCCGCCTTTT-3' **(FRAG. NO:1933) (SEQ. ID NO: 1946)**
5'-GGGCCCBGCCCCGCCGCCTTT-3' **(FRAG. NO:1934) (SEQ. ID NO: 1947) [1945)]**
5'-GGGCCCBGCCCCGCCGCCTT-3' **(FRAG. NO:1935) (SEQ. ID NO: 1948)**
5'-GGGCCCBGCCCCGCCGCCT-3' **(FRAG. NO:1936) (SEQ. ID NO: 1949)**
5'-GGGCCCBGCCCCGCCGCC-3' **(FRAG. NO:1937) (SEQ. ID NO: 1950)**
5'-GGGCCCBGCCCCGCCGC-3' **(FRAG. NO:1938) (SEQ. ID NO: 1951)**
5'-GGGCCCBGCCCCGCCG-3' **(FRAG. NO:1939) (SEQ. ID NO: 1952)**
5'-GGGCCCBGCCCCGCC-3' **(FRAG. NO:1940) (SEQ. ID NO: 1953)**
5'-GGGCCCBGCCCCGC-3' **(FRAG. NO:1941) (SEQ. ID NO: 1954)**
5'-GGGCCCBGCCCCG-3' **(FRAG. NO:1942) (SEQ. ID NO: 1955)**
5'-GGGCCCBGCCCC-3' **(FRAG. NO:1943) (SEQ. ID NO: 1956)**
5'-GGGCCCBGCCC-3' **(FRAG. NO:1944) (SEQ. ID NO: 1957)**
5'-GGCCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1945) (SEQ. ID NO: 1958)**
5'-GCCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1946) (SEQ. ID NO: 1959)**
5'-CCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1947) (SEQ. ID NO: 1960)**
5'-CCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1948) (SEQ. ID NO: 1961)**
5'-CBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1948) (SEQ. ID NO: 1962)**
5'-BGCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1950) (SEQ. ID NO: 1963)**
5'-GCCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1951) (SEQ. ID NO: 1964)**

5'-CCCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1952) (SEQ. ID NO: 1965)**
5'-CCCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1953) (SEQ. ID NO: 1966)**
5'-CCGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1954) (SEQ. ID NO: 1967)**
5'-CGCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1955) (SEQ. ID NO: 1968)**
5'-GCCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1956) (SEQ. ID NO: 1969)**
5'-CCGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1957) (SEQ. ID NO: 1970)**
5'-CGCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1958) (SEQ. ID NO: 1971)**
5'-GCCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1959) (SEQ. ID NO: 1972)**
5'-CCTTTTCTBGCCCCGGC-3' **(FRAG. NO:1960) (SEQ. ID NO: 1973)**
5'-CTTTTCTBGCCCCGGC-3' **(FRAG. NO:1961) (SEQ. ID NO: 1974)**
5'-TTTTCTBGCCCCGGC-3' **(FRAG. NO:1962) (SEQ. ID NO: 1975)**
5'-TTTCTBGCCCCGGC-3' **(FRAG. NO:1963) (SEQ. ID NO: 1976)**
5'-TTCTBGCCCCGGC-3' **(FRAG. NO:1964) (SEQ. ID NO: 1977)**
5'-TCTBGCCCCGGC-3' **(FRAG. NO:1965) (SEQ. ID NO: 1978)**
5'-CTBGCCCCGGC-3' **(FRAG. NO:1966) (SEQ. ID NO: 1979)**
5'-GCGBGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1967) (SEQ. ID NO: 1980)**
5'-GCGBGGCTGTCBCCTCGCTGGGCC-3' **(FRAG. NO:1968) (SEQ. ID NO: 1981)**
5'-GCGBGGCTGTCBCCTCGCTGGGC-3' **(FRAG. NO:1969) (SEQ. ID NO: 1982)**
5'-GCGBGGCTGTCBCCTCGCTGGG-3' **(FRAG. NO:1970) (SEQ. ID NO:1983)**
5'-GCGBGGCTGTCBCCTCGCTGG-3' **(FRAG. NO:1971) (SEQ. ID NO:1984)**
5'-GCGBGGCTGTCBCCTCGCTG-3' **(FRAG. NO:1972) (SEQ. ID NO:1985)**
5'-GCGBGGCTGTCBCCTCGCT-3' **(FRAG. NO:1973) (SEQ. ID NO:1986)**
5'-GCGBGGCTGTCBCCTCGC-3' **(FRAG. NO:1974) (SEQ. ID NO:1987)**
5'-GCGBGGCTGTCBCCTCG-3' **(FRAG. NO:1975) (SEQ. ID NO:1988)**
5'-GCGBGGCTGTCBCCTC-3' **(FRAG. NO:1976) (SEQ. ID NO:1989)**
5'-GCGBGGCTGTCBCCT-3' **(FRAG. NO:1977) (SEQ. ID NO:1990)**
5'-GCGBGGCTGTCBCC-3' **(FRAG. NO:1978) (SEQ. ID NO:1991)**
5'-GCGBGGCTGTCBC-3' **(FRAG. NO:1979) (SEQ. ID NO:1992)**
5'-GCGBGGCTGTCB-3' **(FRAG. NO:1980) (SEQ. ID NO:1993)**
5'-GCGBGGCTGTC-3' **(FRAG. NO:1981) (SEQ. ID NO:1994)**
5'-GCGBGGCTGT-3' **(FRAG. NO:1982) (SEQ. ID NO:1995)**
5'-CGBGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1983) (SEQ. ID NO:1996)**
5'-GBGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1984) (SEQ. ID NO:1997)**
5'-BGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1985) (SEQ. ID NO:1998)**
5'-GGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1986) (SEQ. ID NO:1999)**
5'-GCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1987) (SEQ. ID NO:2000)**
5'-CTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1988) (SEQ. ID NO:2001)**
5'-TGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1989) (SEQ. ID NO:2002)**
5'-GTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1990) (SEQ. ID NO:2003)**
5'-TCBCCTCGCTGGGCCC-3' **(FRAG. NO:1991) (SEQ. ID NO:2004)**
5'-CBCCTCGCTGGGCCC-3' **(FRAG. NO:1992) (SEQ. ID NO:2005)**
5'-BCCTCGCTGGGCCC-3' **(FRAG. NO:1993) (SEQ. ID NO:2006)**
5'-CCTCGCTGGGCCC-3' **(FRAG. NO:1994) (SEQ. ID NO:2007)**
5'-CTCGCTGGGCCC-3' **(FRAG. NO:1995) (SEQ. ID NO:2008)**
5'-TCGCTGGGCCC-3' **(FRAG. NO:1996) (SEQ. ID NO:2009)**
5'-CGCTGGGCCC-3' **(FRAG. NO:1997) (SEQ. ID NO:2010)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:1998) (SEQ. ID NO:2011)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGGG-3' **(FRAG. NO:1999) (SEQ. ID NO:2012)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGG-3' **(FRAG. NO:2000) (SEQ. ID NO:2013)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCG-3' **(FRAG. NO:2001) (SEQ. ID NO:2014)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCC-3' **(FRAG. NO:2002) (SEQ. ID NO:2015)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGC-3' **(FRAG. NO:2003) (SEQ. ID NO:2016)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGG-3' **(FRAG. NO:2004) (SEQ. ID NO:2017)**
5'-GCGCGGCCGTCBTGGCGGCGTCGG-3' **(FRAG. NO:2005) (SEQ. ID NO:2018)**
5'-GCGCGGCCGTCBTGGCGGCGTCG-3' **(FRAG. NO:2006) (SEQ. ID NO:2019)**
5'-GCGCGGCCGTCBTGGCGGCGTC-3' **(FRAG. NO:2007) (SEQ. ID NO:2020)**
5'-GCGCGGCCGTCBTGGCGGCGT-3' **(FRAG. NO:2008) (SEQ. ID NO:2021)**
5'-GCGCGGCCGTCBTGGCGGCG-3' **(FRAG. NO:2009) (SEQ. ID NO:2022)**
5'-GCGCGGCCGTCBTGGCGGC-3' **(FRAG. NO:2010) (SEQ. ID NO:2023)**
5'-GCGCGGCCGTCBTGGCGG-3' **(FRAG. NO:2011) (SEQ. ID NO:2024)**
5'-GCGCGGCCGTCBTGGCG-3' **(FRAG. NO:2012) (SEQ. ID NO:2025)**
5'-GCGCGGCCGTCBTGGC-3' **(FRAG. NO:2013) (SEQ. ID NO:2026)**

5'-GCGCGGCCGTCBTGG-3' **(FRAG. NO:2014) (SEQ. ID NO:2027)**
5'-GCGCGGCCGTCBTG-3' **(FRAG. NO:2015) (SEQ. ID NO:2028)**
5'-GCGCGGCCGTCBT-3' **(FRAG. NO:2016) (SEQ. ID NO:2029)**
5'-GCGCGGCCGTCB-3' **(FRAG. NO:2017) (SEQ. ID NO:2030)**
5'-GCGCGGCCGTC-3' **(FRAG. NO:2018) (SEQ. ID NO:2031)**
5'-GCGCGGCCGT-3' **(FRAG. NO:2019) (SEQ. ID NO:2032)**
5'-CGCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2020) (SEQ. ID NO:2033)**
5'-GCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2021) (SEQ. ID NO:2034)**
5'-CGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2022) (SEQ. ID NO:2035)**
5'-GGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2023) (SEQ. ID NO:2036)**
5'-GCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2024) (SEQ. ID NO:2037)**
5'-CCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2025) (SEQ. ID NO:2038)**
5'-CGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2026) (SEQ. ID NO:2039)**
5'-GTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2027) (SEQ. ID NO:2040)**
5'-TCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2028) (SEQ. ID NO:2041)**
5'-CBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2029) (SEQ. ID NO:2042)**
5'-BTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2030) (SEQ. ID NO:2043)**
5'-TGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2031) (SEQ. ID NO:2044)**
5'-GGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2032) (SEQ. ID NO:2045)**
5'-GCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2033) (SEQ. ID NO:2046)**
5'-CGGCGTCGGGCCGGGC-3' **(FRAG. NO:2034) (SEQ. ID NO:2047)**
5'-GGCGTCGGGCCGGGC-3' **(FRAG. NO:2035) (SEQ. ID NO:2048)**
5'-GCGTCGGGCCGGGC-3' **(FRAG. NO:2036) (SEQ. ID NO:2049)**
5'-CGTCGGGCCGGGC-3' **(FRAG. NO:2037) (SEQ. ID NO:2050)**
5'-GTCGGGCCGGGC-3' **(FRAG. NO:2038) (SEQ. ID NO:2051)**
5'-TCGGGCCGGGC-3' **(FRAG. NO:2039) (SEQ. ID NO:2052)**
5'-CGGGCCGGGC-3' **(FRAG. NO:2040) (SEQ. ID NO:2053)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2041) (SEQ. ID NO:2054)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCC-3' **(FRAG. NO:2042) (SEQ. ID NO:2055)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGC-3' **(FRAG. NO:2043) (SEQ. ID NO:2056)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGG-3' **(FRAG. NO:2044) (SEQ. ID NO:2057)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGG-3' **(FRAG. NO:2045) (SEQ. ID NO:2058)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCG-3' **(FRAG. NO:2046) (SEQ. ID NO:2059)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGCC-3' **(FRAG. NO:2047) (SEQ. ID NO:2060)**
5'-CCGCBGGCCBGGGCGCGCCGCCGGC-3' **(FRAG. NO:2048) (SEQ. ID NO:2061)**
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' **(FRAG. NO:2049) (SEQ. ID NO:2062)**
5'-CCGCBGGCCBGGGCGCGCCGCCG-3' **(FRAG. NO:2050) (SEQ. ID NO:2063)**
5'-CCGCBGGCCBGGGCGCGCCGCC-3' **(FRAG. NO:2051) (SEQ. ID NO:2064)**
5'-CCGCBGGCCBGGGCGCGCCGC-3' **(FRAG. NO:2052) (SEQ. ID NO:2065)**
5'-CCGCBGGCCBGGGCGCGCCG-3' **(FRAG. NO:2053) (SEQ. ID NO:2066)**
5'-CCGCBGGCCBGGGCGCGCC-3' **(FRAG. NO:2054) (SEQ. ID NO:2067)**
5'-CCGCBGGCCBGGGCGCGC-3' **(FRAG. NO:2055) (SEQ. ID NO:2068)**
5'-CCGCBGGCCBGGGCGCG-3' **(FRAG. NO:2056) (SEQ. ID NO:2069)**
5'-CCGCBGGCCBGGGCGC-3' **(FRAG. NO:2057) (SEQ. ID NO:2070)**
5'-CCGCBGGCCBGGGCG-3' **(FRAG. NO:2058) (SEQ. ID NO:2071)**
5'-CCGCBGGCCBGGGC-3' **(FRAG. NO:2059) (SEQ. ID NO:2072)**
5'-CCGCBGGCCBGGG-3' **(FRAG. NO:2060) (SEQ. ID NO:2073)**
5'-CCGCBGGCCBGG-3' **(FRAG. NO:2061) (SEQ. ID NO:2074)**
5'-CCGCBGGCCBG-3' **(FRAG. NO:2062) (SEQ. ID NO:2075)**
5'-CCGCBGGCCB-3' **(FRAG. NO:2063) (SEQ. ID NO:2076)**
5'-CCGCBGGCC-3' **(FRAG. NO:2064) (SEQ. ID NO:2077)**
5'-CGCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2065) (SEQ. ID NO:2078)**
5'-GCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2066) (SEQ. ID NO:2079)**
5'-CBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2067) (SEQ. ID NO:2080)**
5'-BGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2068) (SEQ. ID NO:2081)**
5'-GGCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2069) (SEQ. ID NO:2082)**
5'-GCCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2070) (SEQ. ID NO:2083)**
5'-CCBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2071) (SEQ. ID NO:2084)**
5'-CBGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2072) (SEQ. ID NO:2085)**
5'-BGGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2073) (SEQ. ID NO:2086)**
5'-GGGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2074) (SEQ. ID NO:2087)**
5'-GGCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2075) (SEQ. ID NO:2088)**

5'-GCGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2076) (SEQ. ID NO:2089)**
5'-CGCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2077) (SEQ. ID NO:2090)**
5'-GCGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2078) (SEQ. ID NO:2091)**
5'-CGCCGCCGGCCGGGCCG-3' **(FRAG. NO:2079) (SEQ. ID NO:2092)**
5'-GCCGCCGGCCGGGCCG-3' **(FRAG. NO:2080) (SEQ. ID NO:2093)**
5'-CCGCCGGCCGGGCCG-3' **(FRAG. NO:2081) (SEQ. ID NO:2094)**
5'-CGCCGGCCGGGCCG-3' **(FRAG. NO:2082) (SEQ. ID NO:2095)**
5'-GCCGGCCGGGCCG-3' **(FRAG. NO:2083) (SEQ. ID NO:2096)**
5'-CCGGCCGGGCCG-3' **(FRAG. NO:2084) (SEQ. ID NO:2097)**
5'-CGGCCGGGCCG-3' **FRAG. NO:2085) (SEQ. ID NO:2098)**
5'-GGCCGGGCCG-3' **(FRAG. NO:2086) (SEQ. ID NO:2099)**
5'-GGGCGCBGGCTCCGCB-3' **(FRAG. NO:2087) (SEQ. ID NO:2100)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3'**(FRAG.NO:2088)(SEQ.ID NO:2101)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' **(FRAG.NO:2089)(SEQ.ID NO:2102)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCC-3' **(FRAG.NO:2090)(SEQ.ID NO:2103)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCC-3' **(FRAG. NO:2091) (SEQ. ID NO:2104)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGC-3' **(FRAG. NO:2092) (SEQ. ID NO:2105)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGG-3' **(FRAG. NO:2093) (SEQ. ID NO:2106)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCG-3' **(FRAG. NO:2094) (SEQ. ID NO:2107)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCC-3' **(FRAG. NO:2095) (SEQ. ID NO:2108)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCC-3' **(FRAG. NO:2096) (SEQ. ID NO:2109)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGC-3' **(FRAG. NO:2097) (SEQ. ID NO:2110)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCG-3' **(FRAG. NO:2098) (SEQ. ID NO:2111)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCC-3' **(FRAG. NO:2099) (SEQ. ID NO:2112)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCC-3' **(FRAG. NO:2100) (SEQ. ID NO:2113)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGC-3' **(FRAG. NO:2101) (SEQ. ID NO:2114)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTG-3' **(FRAG. NO:2102) (SEQ. ID NO:2115)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTT-3' **(FRAG. NO:2103) (SEQ. ID NO:2116)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCT-3' **(FRAG. NO:2104) (SEQ. ID NO:2117)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGC-3' **(FRAG. NO:2105) (SEQ. ID NO:2118)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGG-3' **(FRAG. NO:2106) (SEQ. ID NO:2119)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCG-3' **(FRAG. NO:2107) (SEQ. ID NO:2120)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCCC-3' **(FRAG. NO:2108) (SEQ. ID NO:2121)**
5'-GGGCCCCTGGCTCGGCCCCGCGGCC-3' **(FRAG. NO:2109) (SEQ. ID NO:2122)**
5'-GGGCCCCTGGCTCGGCCCCGCGGC-3' **(FRAG. NO:2110) (SEQ. ID NO:2123)**
5'-GGGCCCCTGGCTCGGCCCCGCGG-3' **(FRAG. NO:2111) (SEQ. ID NO:2124)**
5'-GGGCCCCTGGCTCGGCCCCGCG-3' **(FRAG. NO:2112) (SEQ. ID NO:2125)**
5'-GGGCCCCTGGCTCGGCCCCGC-3' **(FRAG. NO:2113) (SEQ. ID NO:2126)**
5'-GGGCCCCTGGCTCGGCCCCG-3' **(FRAG. NO:2114) (SEQ. ID NO:2127)**
5'-GGGCCCCTGGCTCGGCCCC-3' **(FRAG. NO:2115) (SEQ. ID NO:2128)**
5'-GGGCCCCTGGCTCGGCCC-3' **(FRAG. NO:2116) (SEQ. ID NO:2129)**
5'-GGGCCCCTGGCTCGGCC-3' **(FRAG. NO:2117) (SEQ. ID NO:2130)**
5'-GGGCCCCTGGCTCGGC-3' **(FRAG. NO:2118) (SEQ. ID NO:2131)**
5'-GGGCCCCTGGCTCGG-3' **(FRAG. NO:2119) (SEQ. ID NO:2132)**
5'-GGGCCCCTGGCTCG-3' **(FRAG. NO:2120) (SEQ. ID NO:2133)**
5'-GGGCCCCTGGCTC-3' **(FRAG. NO:2121) (SEQ. ID NO:2134)**
5'-GGGCCCCTGGCT-3' **(FRAG. NO:2122) (SEQ. ID NO:2135)**
5'-GGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3'**(FRAG.NO:2123)(SEQ.ID NO:2136)**
5'-GCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2124) (SEQ. ID NO:2137)**
5'-CCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2125) (SEQ. ID NO:2138)**
5'-CCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2126) (SEQ. ID NO:2139)**
5'-CCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2127) (SEQ. ID NO:2140)**
5'-CTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2128) (SEQ. ID NO:2141)**
5'-TGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2129) (SEQ. ID NO:2142)**
5'-GGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2130) (SEQ. ID NO:2143)**
5'-GCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2131) (SEQ. ID NO:2144)**
5'-CTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2132) (SEQ. ID NO:2145)**
5'-TCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2133) (SEQ. ID NO:2146)**
5'-CGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2134) (SEQ. ID NO:2147)**
5'-GGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2135) (SEQ. ID NO:2148)**
5'-GCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2136) (SEQ. ID NO:2149)**
5'-CCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2137) (SEQ. ID NO:2150)**

5'-CCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2138) (SEQ. ID NO:2151)**
5'-CCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2139) (SEQ. ID NO:2152)**
5'-CGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2140) (SEQ. ID NO:2153)**
5'-GCGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2141) (SEQ. ID NO:2154)**
5'-CGGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2142) (SEQ. ID NO:2155)**
5'-GGCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2143) (SEQ. ID NO:2156)**
5'-GCCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2144) (SEQ. ID NO:2157)**
5'-CCCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2145) (SEQ. ID NO:2158)**
5'-CCGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2146) (SEQ. ID NO:2159)**
5'-CGGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2147) (SEQ. ID NO:2160)**
5'-GGCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2148) (SEQ. ID NO:2161)**
5'-GCTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2149) (SEQ. ID NO:2162)**
5'-CTTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2150) (SEQ. ID NO:2163)**
5'-TTGCCCGCCCGGCCCGG-3' **(FRAG. NO:2151) (SEQ. ID NO:2164)**
5'-TGCCCGCCCGGCCCGG-3' **(FRAG. NO:2152) (SEQ. ID NO:2165)**
5'-GCCCGCCCGGCCCGG-3' **(FRAG. NO:2153) (SEQ. ID NO:2166)**
5'-CCCGCCCGGCCCGG-3' **(FRAG. NO:2154) (SEQ. ID NO:2167)**
5'-CCGCCCGGCCCGG-3' **(FRAG. NO:2155) (SEQ. ID NO:2168)**
5'-CGCCCGGCCCGG-3' **(FRAG. NO:2156) (SEQ. ID NO:2169)**
5'-GCCCGGCCCGG-3' **(FRAG. NO:2157) (SEQ. ID NO:2170)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2158) (SEQ. ID NO:2171)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCC-3' **(FRAG. NO:2159) (SEQ. ID NO:2172)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCC-3' **(FRAG. NO:2160) (SEQ. ID NO:2173)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGC-3' **(FRAG. NO:2161) (SEQ. ID NO:2174)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGG-3' **(FRAG. NO:2162) (SEQ. ID NO:2175)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGG-3' **(FRAG. NO:2163) (SEQ. ID NO:2176)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBG-3' **(FRAG. NO:2164) (SEQ. ID NO:2177)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTB-3' **(FRAG. NO:2165) (SEQ. ID NO:2178)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCT-3' **(FRAG. NO:2166) (SEQ. ID NO:2179)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCC-3' **(FRAG. NO:2167) (SEQ. ID NO:2180)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCGC-3' **(FRAG. NO:2168) (SEQ. ID NO:2181)**
5'-GGCGGGGGCGGCGGCGCCTGGCTCG-3' **(FRAG. NO:2169) (SEQ. ID NO:2182)**
5'-GGCGGGGGCGGCGGCGCCTGGCTC-3' **(FRAG. NO:2170) (SEQ. ID NO:2183)**
5'-GGCGGGGGCGGCGGCGCCTGGCT-3' **(FRAG. NO:2171) (SEQ. ID NO:2184)**
5'-GGCGGGGGCGGCGGCGCCTGGC-3' **(FRAG. NO:2172) (SEQ. ID NO:2185)**
5'-GGCGGGGGCGGCGGCGCCTGG-3' **(FRAG. NO:2173) (SEQ. ID NO:2186)**
5'-GGCGGGGGCGGCGGCGCCTG-3' **(FRAG. NO:2174) (SEQ. ID NO:2187)**
5'-GGCGGGGGCGGCGGCGCCT-3' **(FRAG. NO:2175) (SEQ. ID NO:2188)**
5'-GGCGGGGGCGGCGGCGCC-3' **(FRAG. NO:2176) (SEQ. ID NO:2189)**
5'-GGCGGGGGCGGCGGCGC-3' **(FRAG. NO:2177) (SEQ. ID NO:2190)**
5'-GGCGGGGGCGGCGGCG-3' **(FRAG. NO:2178) (SEQ. ID NO:2191)**
5'-GGCGGGGGCGGCGGC-3' **(FRAG. NO:2179) (SEQ. ID NO:2192)**
5'-GGCGGGGGCGGCGG-3' **(FRAG. NO:2180) (SEQ. ID NO:2193)**
5'-GGCGGGGGCGGCG-3' **(FRAG. NO:2181) (SEQ. ID NO:2194)**
5'-GGCGGGGGCGGC-3' **(FRAG. NO:2182) (SEQ. ID NO:2195)**
5'-GGCGGGGGCGG-3' **(FRAG. NO:2183) (SEQ. ID NO:2196)**
5'-GCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2184) (SEQ. ID NO:2197)**
5'-CGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2185) (SEQ. ID NO:2198)**
5'-GGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2186) (SEQ. ID NO:2199)**
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2187) (SEQ. ID NO:2200)**
5'-GGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2188) (SEQ. ID NO:2201)**
5'-GGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2189) (SEQ. ID NO:2202)**
5'-GCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2190) (SEQ. ID NO:2203)**
5'-CGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2191) (SEQ. ID NO:2204)**
5'-GGCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2192) (SEQ. ID NO:2205)**
5'-GCGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2193) (SEQ. ID NO:2206)**
5'-CGGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2194) (SEQ. ID NO:2207)**
5'-GGCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2195) (SEQ. ID NO:2208)**
5'-GCGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2196) (SEQ. ID NO:2209)**
5'-CGCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2197) (SEQ. ID NO:2210)**
5'-GCCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2198) (SEQ. ID NO:2211)**
5'-CCTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2199) (SEQ. ID NO:2212)**

5'-CTGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2200) (SEQ. ID NO:2213)**
5'-TGGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2201) (SEQ. ID NO:2214)**
5'-GGCTCGCCTBGGGCCCC-3' **(FRAG. NO:2202) (SEQ. ID NO:2215)**
5'-GCTCGCCTBGGGCCCC-3' **(FRAG. NO:2203) (SEQ. ID NO:2216)**
5'-CTCGCCTBGGGCCCC-3' **(FRAG. NO:2204) (SEQ. ID NO:2217)**
5'-TCGCCTBGGGCCCC-3' **(FRAG. NO:2205) (SEQ. ID NO:2218)**
5'-CGCCTBGGGCCCC-3' **(FRAG. NO:2206) (SEQ. ID NO:2219)**
5'-GCCTBGGGCCCC-3 **(FRAG. NO:2207) (SEQ. ID NO:2220)**
5'-CCTBGGGCCCC-3' **(FRAG. NO:2208) (SEQ. ID NO:2221)**
5'-CTBGGGCCCC-3' **(FRAG. NO:2209) (SEQ. ID NO:2222)**
5'-GGGTGGGCBCGGCGGCC-3' **(FRAG. NO:2210) (SEQ. ID NO:2223)**
5'-GGTCGGCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2211) (SEQ. ID NO:2224)**
5'-GGTCGGCGBBGBGCTCGTCGTGG-3' **(FRAG. NO:2212) (SEQ. ID NO:2225)**
5'-GGTCGGCGBBGBGCTCGTCGTG-3' **(FRAG. NO:2213) (SEQ. ID NO:2226)**
5'-GGTCGGCGBBGBGCTCGTCGT-3' **(FRAG. NO:2214) (SEQ. ID NO:2227)**
5'-GGTCGGCGBBGBGCTCGTCG-3' **(FRAG. NO:2215) (SEQ. ID NO:2228)**
5'-GGTCGGCGBBGBGCTCGTC-3' **(FRAG. NO:2216) (SEQ. ID NO:2229)**
5'-GGTCGGCGBBGBGCTCGT-3' **(FRAG. NO:2217) (SEQ. ID NO:2230)**
5'-GGTCGGCGBBGBGCTCG-3' **(FRAG. NO:2218) (SEQ. ID NO:2231)**
5'-GGTCGGCGBBGBGCTC-3' **(FRAG. NO:2219) (SEQ. ID NO:2232)**
5'-GGTCGGCGBBGBGCT-3' **(FRAG. NO:2220) (SEQ. ID NO:2233)**
5'-GGTCGGCGBBGBGC-3' **(FRAG. NO:2221) (SEQ. ID NO:2234)**
5'-GGTCGGCGBBGBG-3' **(FRAG. NO:2222) (SEQ. ID NO:2235)**
5'-GGTCGGCGBBGB-3' **(FRAG. NO:2223) (SEQ. ID NO:2236)**
5'-GGTCGGCGBBG-3' **(FRAG. NO:2224) (SEQ. ID NO:2237)**
5'-GTCGGCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2225) (SEQ. ID NO:2238)**
5'-TCGGCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2226) (SEQ. ID NO:2239)**
5'-CGGCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2227) (SEQ. ID NO:2240)**
5'-GGCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2228) (SEQ. ID NO:2241)**
5'-GCGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2229) (SEQ. ID NO:2242)**
5'-CGBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2230) (SEQ. ID NO:2243)**
5'-GBBGBGCTCGTCGTGGC-3' **(FRAG. NO:2231) (SEQ. ID NO:2244)**
5'-BBGBGCTCGTCGTGGC-3' **(FRAG. NO:2232) (SEQ. ID NO:2245)**
5'-BGBGCTCGTCGTGGC-3' **(FRAG. NO:2233) (SEQ. ID NO:2246)**
5'-GBGCTCGTCGTGGC-3' **(FRAG. NO:2234) (SEQ. ID NO:2247)**
5'-BGCTCGTCGTGGC-3' **(FRAG. NO:2235) (SEQ. ID NO:2248)**
5'-GCTCGTCGTGGC-3' **(FRAG. NO:2236) (SEQ. ID NO:2249)**
5'-CTCGTCGTGGC-3' **(FRAG. NO:2237) (SEQ. ID NO:2250)**
5'-TCGTCGTGGC-3' **(FRAG. NO:2238) (SEQ. ID NO:2251)**
5'-GGGGCCCCGCGCCGCCCGCC-3' **(FRAG. NO:2239) (SEQ. ID NO:2252)**
5'-GGGGCCCCGCGCCGCCCGC-3' **(FRAG. NO:2240) (SEQ. ID NO:2253)**
5'-GGGGCCCCGCGCCGCCCG-3' **(FRAG. NO:2241) (SEQ. ID NO:2254)**
5'-GGGGCCCCGCGCCGCCC-3' **(FRAG. NO:2242) (SEQ. ID NO:2255)**
5'-GGGGCCCCGCGCCGCC-3' **(FRAG. NO:2243) (SEQ. ID NO:2256)**
5'-GGGGCCCCGCGCCGC-3' **(FRAG. NO:2244) (SEQ. ID NO:2257)**
5'-GGGGCCCCGCGCCG-3' **(FRAG. NO:2245) (SEQ. ID NO:2258)**
5'-GGGGCCCCGCGCC-3' **(FRAG. NO:2246) (SEQ. ID NO:2259)**
5'-GGGGCCCCGCGC-3 **(FRAG. NO:2247) (SEQ. ID NO:2260)**
5'-GGGCCCCGCGCCGCCCGCC-3' **(FRAG. NO:2248) (SEQ. ID NO:2261)**
5'-GGCCCCGCGCCGCCCGCC-3' **(FRAG. NO:2249) (SEQ. ID NO:2262)**
5'-GCCCCGCGCCGCCCGCC-3' **(FRAG. NO:2250) (SEQ. ID NO:2263)**
5'-CCCCGCGCCGCCCGCC-3' **(FRAG. NO:2251) (SEQ. ID NO:2264)**
5'-CCCGCGCCGCCCGCC-3' **(FRAG. NO:2252) (SEQ. ID NO:2265)**
5'-CCGCGCCGCCCGCC-3' **(FRAG. NO:2253) (SEQ. ID NO:2266)**
5'-CGCGCCGCCCGCC-3' **(FRAG. NO:2254) (SEQ. ID NO:2267)**
5'-GCGCCGCCCGCC-3' **(FRAG. NO:2255) (SEQ. ID NO:2268)**
5'-CGCCGCCCGCC-3' **(FRAG. NO:2256) (SEQ. ID NO:2269)**
5'-GCCGCCCGCC-3' **(FRAG. NO:2257) (SEQ. ID NO:2270)**
5'-GGGGCGCGCGGGGCCGCCGGG-3' **(FRAG. NO:2258) (SEQ. ID NO:2271)**
5'-GGCGGGGBGCGGCBGGGCCCGGGCCC-3' **(FRAG. NO:2259) (SEQ. ID NO:2272)**
5'-GGCGCGTCGCCGTCGCCCCBGTCGGGCTCGCGC-3' **(FRAG. NO:2260) (SEQ. ID NO:2273)**
5'-GCGCGGGCBBCBGCGBGCCGGGCGCG-3' **(FRAG. NO:2261) (SEQ. ID NO:2274)**

5'-GCGCBCGGGCCCBCCTGCGCGGGC-3' **(FRAG. NO:2262) (SEQ. ID NO:2275)**
5'-GGGCGGGGTGGGCTGCCCTGCGGCCGCC-3' **(FRAG. NO:2263) (SEQ. ID NO:2276)**
5'-GGGCTGCTGCGCGGCGGCTCCGGCGA-3' **(FRAG. NO:2264) (SEQ. ID NO:2277)**
5'-CTCCCGGGCGGGGCCGGGCGCGGGG-3' **(FRAG. NO:2265) (SEQ. ID NO:2278)**
5'-GGGCTGCCGCGGTCCGGGCCCCTCTTGCCGGCG-3' **(FRAG. NO:2266) (SEQ. ID NO:2279)**
5'-GCGCTCGCGCCGCTGCCGG-3' **(FRAG. NO:2267) (SEQ. ID NO:2280)**
5'-GCGCCGCTTGGCCTTGTCGCGGC-3' **(FRAG. NO:2268) (SEQ. ID NO:2281)**
5'-GCTGCTCCBCGCGCTGG-3' **(FRAG. NO:2269) (SEQ. ID NO:2282)**
5'-GCCGGBGGCCGGCCBGGTCCCGCG-3' **(FRAG. NO:2270) (SEQ. ID NO:2283)**
5'-CCCGGCGGCCGGCGGGBBGGGCGGGCTGGGC-3' **(FRAG. NO:2271) (SEQ. ID NO:2284)**
5'-GTCTCTCCCGCCCCGGCCGCGCG-3' **(FRAG. NO:2272) (SEQ. ID NO:2285)**
5'-GGGCGTCCGCTCCGGGCCGTCGGG-3' **(FRAG. NO:2273) (SEQ. ID NO:2286)**
5'-GCGGGCACGCGGCGGCTCTGGCGTCGGC-3' **(FRAG. NO:2274) (SEQ. ID NO:2287)**

<u>Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-GGTGBCBTTG BGCBTGTCGG CGCGGTCCCG TTBBGBGTGG GCCCGCCAGC CCAGCCACTC CACTTGGGGG
CGGGTGGCCA GCACGAACAG CACCCAGAGG AAGGGGGGCG GCCCAGAAGG GCAGCCCGCA GGCCAGGATC
AGGTCTGCTG CGGCCGGAGA TAATGGCATT CACCACGCGG CGGCCCAGCG CACGCCGCGC ATCCGGCCCG
GGTTCTGACC TGCAGCCCCC GTCTCCTTGG CATTCCTGGG CCCCAGTCAC TCCTCTCCCT GCCCCCCTTG
CTGGGGCAGG GACGGGGTG BCBTTGBGCB TGTCGGCGCG GTCCCGTTBB GBGTGGGCCC GCCAGCCCAG
CCACTCCACT TGGGGGCGGG TGGCCAGCAC GAACAGCACC CAGAGGAAGG GGGGCGGCCC AGAAGGGCAG
CCCGCAGGCC AGGATCAGGT CTGCTGCGGC CGGAGATAAT GGCATTCACC ACGCGGCGGC CCAGCGCACG
CCGCGCATCC GGCCCGGGTT CTGACCTGCA GCCCCCGTCT CCTTGGCATT CCTGGGCCCC AGTCACTCCT
CTCCCTGCCC CCCTTGCTGG GGCAGGGACG GCCGTGTTGT CBGTGGTGCT GCCCGTTTGB GGTBTGGCGC
TCCBCCBBTT CCCTTTCTC CTTGTTTTCC GTTTCTCTTG CCGTCTGTGG TT CAGATTCACA AACTGCAGGA
CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA
GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG
TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG
GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT
GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC
CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT
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5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG-3' **(FRAG.NO:2275) (SEQ.ID NO:2461)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2460)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTTCCCT GTGGTCGTGG GGAGTT-3' **(FRAG.NO:2275)(SEQ. ID NO:2459)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC

CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC
ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2458)**
5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCCTCTT
TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT
CTCCAACAAC TTCCACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC
ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2457)**
5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG
CTGCAAAGTC CCCACCCTCC CTCGCCATCT GTATCCTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT
ACGGAAATAC GATCCCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA
GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT CTCTTTTAAT AAATTAACTC ACCCACCACA
CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCCGGTT GATAAGGAAG GAATGTGAAT
CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG TTGGTGGATA
CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG
GCTTCTCCTT GCCCTGGCTG GTTGTCCTTA ACCCCTGTCT CCTTCTGGAC CAGTTTTTGT CCTTCCCTTG
TGACCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG
GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT
TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG CAGACCTGAT
CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG
CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA
GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA
GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG
AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG
TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT
GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC
ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC
TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC
AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA
CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA
GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTTGA
TGTCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT
GGGGTGAACT CACCCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT GCTGCCACAC
CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT GAGCTTCCCT
CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACTTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG

TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG TATTGAGCAC TGTAGGCA -3' **(FRAG. NO:2275) (SEQ. ID NO:2456)**

5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC CTTCTGGACC AGTTTTTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGCACAT ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTC TTCTGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3' **(FRAG. NO:2275) (SEQ. ID NO:2455)**

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAAAAA AAAAAAAAAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG TTTGAATTCC CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCCGGTGTT GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG GGAGTGATGT GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAAATAC TCACATGTGT CTGTCTCCCT TATTAGGTTC AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCCTG CTGGACCCAA CCAGCCCTAT GGGGTCGCAT CCCCACCTGC CTGGAATTCT CCAAAGAACC TCCCCTTTAA CAGTTCCAGC CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCCTCT AAATCAGCCC CCCATCTCTG CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG TCAGGTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG TCCTTGCTTC CACTCTACCC CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG CCAACCTGAC TGACATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT

TCTCATCAAT AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTC TATGCTCTCA CAGGACCTTT
TGCTTGATTT TTCACTGTAC TTAGGTCAGT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA
GTAGACTGTC AGCTCCTAGC CATTGTATAC CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG
AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG AGAATGCGTG TATTTGGCAA TCCCCAGCCC
CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC ACTCACATCC CACTCTGAGT
CCAAATGTTC TCTCCCTGGA AGATATCAAT GTTTCTGTCT GTTCGTGAGG ACTCCGTGCC CACCACGGCC
TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAACT
CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC
AAAACCTCTC AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA
AGAGGGGCTC AGGGAGGAGA AGGGCACATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACTTG
GAAGTGAAGG GAAGAGAGTT AAACATTAAA GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC
CTTGGAAACA AAATATCTCC AACACATGGC TGACATTTGG TGGGAGATCA GAACACCCTA AAGAGAGAAT
TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC AGAGGATAGG GAGATCTGTT CTTGGGGACA
GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCCACCCTG CTGCAGGTGC TGCCTATGAT
GAAGATGAGC AGATGGCCAT CTCAGCTGGG GCCACAGTGC ACTGGACCTA TAGTTTCCAA TTCCGCACTC
AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT
ACTGTCTTGC TGACAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA
AAGATGATAG ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA
GGGTTGGACC AAGGGACTAC CCAGGGGAAG TCTTACCTTC AGAGGACTCT GGAAAGGAGG CTGCAAGTTT
TCATGGGTCA AGAATTCAGA GCCCAGTAGA GACAGCTTAT CTCTGTTCCA AGATGTCTGG GGCCTTGGTT
GGAAGATTCA AAGGCTAGGA AACCAGGAGC CACCAAAAGC GTAACTGGGG CCAGAGGATC CACTTTCAAG
GTGGCAAGTT GGTTCCCCCC ATGTGGCTGC TTGAGTATCC TCACATGGCG GCTCACATCC TTCCAAGTAA
GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC ACACCATCCC
TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT TTGAAATGAA
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTTAG AGCATACTTC
TTATACCATC ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA
CGCTTACTCC CTCACTCAAC CTCTTGCTAC TTCCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG
AACATACCAA CAGCTTCCCC AGTTCTGTGC CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCCT
CCTTCTTGTC CGGTCAAAAT GCTTCTTATC CTTCAAGACC CAGCTCTAGA GTCACCTCCA ACCCCTTACC
CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCCCT GCTCCCTCCA GGGCACCCTC CACCCTCTGG
GCCACAGTTG TCACGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTTG CACTCAGGGC
AGAGCTCAGC ACACAGCAGA CGCTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GGTCCCCCAG
TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA
TGATCAGTAA TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC
CAGAAAGAGC CCCTTTTCCT TCTCTCACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC
TCTGGGTTGT GCTTTGGACT TTTCAGTGTG TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT
GAAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC CCTACTCCAA AGAAGGCAAC ATAGAAGCTC
AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAACTCA TGGCTGTCCA AGCCCCATGC
CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT CTGTGAGTCT
TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC
CACTGATAAT AAGCGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT
TGCACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT ACAGGTGAGG
TCATTGTGGT TCAAGGACGT TAAGTAACTT CCCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG
TGAACCCAGT AGGACTATCT GGCTGCAAAG TCCCCACCCC CCTCGCCATC TGTATCCTCC AATCACTTCA
GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA CAGACTGTCC AGGAAGACAG AAACTAGGCA
GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAATCTCC AGGTCTGGAA TGATATCATT TTTCTCTTTT
AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG GAGGGCCCCG
GTTGATAAGG AAGCAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG
ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG
GCCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG
GGCATGCAGA AAACAGCCTG AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT
CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT
CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC
CCCCAAGTGG AGTCGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCCT CTGGGTGCTG TTCGTGCTGG
CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC AGCTGCACGG TGGCAGAGAT
CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC
TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC
TGTACAGCAG CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC
CATGGGCCGG ATGCGCGGCG TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC
CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT
GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC CTGAATGTCG TGGGCTTCCT
GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC TGCGGAACAA CGAGATGCAG

AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCATCA
TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC
AACCCACTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT
GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT
CTCCGTGGAA CGCCAGATTC ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG
GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA
CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC
CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA
ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT
GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT
AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG
TTTCTTTAAT CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG
GTCCCTGATA ACAACCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA
AAGAAGAATC CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG
AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC
ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA
GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' **(FRAG. NO:2275) (SEQ. ID NO:2454)**

5'- CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT
TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA
CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG
GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT
TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA
GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG
AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA
TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA
ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA
TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG
AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC
TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA
GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT
GTGAGGGTTA AAGCCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA
TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT
GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT
TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG
AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG
AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG
GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT
ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA
TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC
TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC
TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA
ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG
GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT
AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC
AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG
CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA
AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA
AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT
ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA
CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG
CACCAGAGCA CGTCATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC
ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT
AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA
CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA
AAAAAAAAA -3' **(FRAG. NO:2275) (SEQ. ID NO:2453)**

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT
CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC
AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG
AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC
TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT
TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC

CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG
TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT
AGTAAGTCTT TGACCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC
TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC
ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC
CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC
AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC
ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA
CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG
AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA
CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC
CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT
GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA
GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG-3'
(FRAG..NO:2275) (SEQ.ID NO:2452)

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG
CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC
CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3'
(FRAG.NO:2275) (SEQ.ID NO:2451)

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
CGGTGGGGAC ATCAGGCTGC CCCGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGGAGA
AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG
AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTTCCCT GTGGTCGTGG GGAGTT-3' **(FRAG.NO:2275) (SEQ. ID NO:2450)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC ACGGCCTCTT
TCAGCGCCGA CATCCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT
CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC
ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2449)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCCTCTT
TCAGCGCCGA CATCCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT
CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC
ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2448)**

5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG
CTGCAAAGTC CCCACCCTCC CTCGCCATCT GTATCCTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT
ACGGAAATAC GATGCCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA
GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT CTCTTTTAAT AAATTAACTC ACCCACCACA
CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCCGGTT GATAAGGAAG GAATGTGAAT
CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG TTGGTGGATA
CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG
GCTTCTCCTT GCCCTGGCTG GTTGTCCTTA ACCCCTGTCT CCTTCTGGAC CAGTTTTTGT CCTTCCCTTG
TGACCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG
GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT
TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG CAGACCTGAT
CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG
CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA
GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA
GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG
AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG
TGTTCACCAA CATCCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT
GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC
ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC
TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC
AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA
CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA
GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTTGA
TGTCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT
GGGGTGAACT CACCCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT GCTGCCACAC
CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT GAGCTTCCCT
CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACTTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG
TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG
ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT
ATGGCTCCCC TCACTGATGG ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC
TGTATATCAG TATTGAGCAC TGTAGGCA -3' **(FRAG. NO:2275) (SEQ. ID NO:2447)**

5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC
CTTCTGGACC AGTTTTTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG
CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC
CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA
CCTGGGGAAC CTGCCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC
AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT
ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT
GGGCCGGATG CGCCGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG
AGCTCACCCA TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG
TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT
GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT
GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA
GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC
CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC
CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT
GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT
CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA
ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA
GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG
GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA
TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT
CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC
CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA

GAAGAATCCA ATAAGCACAT ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA
GAAAGAGAAG GAGCCATCTC CATCTTGAAG GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC
ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC
CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTC TTCTGTAACA
TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC
ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'

(FRAG. NO:2275) (SEQ. ID NO:2446)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC
ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT
GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG
TGATCCCAGC TACTCAGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC
AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAAAAA AAAAAAAAAA
AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC
TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT TCAGAAGGAC
TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA
ACCTTTTCCA GGTCTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG
TTTGAATTCC CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG
AAACCCAGGT GCCCGGTGTT GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC
ACACACACAC ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC
ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT GTGAAGTCCT
GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA CAAGTCACCA CCAACCCATC
TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG GGAGTGATGT
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ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA
GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC-3' **(FRAG.NO:2275) (SEQ. D NO:2445)**
5'-CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT
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TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG
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GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGCCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG CACCAGAGCA CGTCATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAAA-3' **(FRAG. NO:2275) (SEQ. ID NO:2444)**

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGCACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGCCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG-3' **(FRAG.NO:2275) (SEQ. ID NO:2443)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2442)**

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAAAAA AAAAAAAAAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA ACCTTTTCCA GGTCTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG

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GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG
ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG
GCCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG
GGCATGCAGA AAACAGCCTG AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT
CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT
CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC
CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCCT CTGGGTGCTG TTCGTGCTGG
CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC AGCTGCACGG TGGCAGAGAT
CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC
TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC
TGTACAGCAG CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC
CATGGGCCGG ATGCGCGGCG TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC
CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT
GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC CTGAATGTCG TGGGCTTCCT
GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC TGCGGAACAA CGAGATGCAG
AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCATCA
TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC
AACCCACTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT
GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT
CTCCGTGGAA CGCCAGATTC ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG
GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA
CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC
CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA
ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT
GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT
AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG
TTTCTTTAAT CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG
GTCCCTGATA ACAACCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA
AAGAAGAATC CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG
AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC
ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA
GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' **(FRAQ. NO: _) (SEQ. ID NO 2441)**

5'-CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT
TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA
CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG
GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT
TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA
GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG
AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA
TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA
ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA
TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG
AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC
TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA
GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT
GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA
TCATTACGCA GACCTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT
GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT
TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG
AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG
AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG
GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT
ATGAGCCCTA GAACAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA
TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC
TAGAACCTGG AGGCCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC
TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA
ACCTGGAGGG CTGCAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG
GCTAGAACCT GGACGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT
AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC
AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG

CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG CACCAGAGCA CGTCATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAAA -3' **(FRAQ. NO: _) (SEQ. ID NO 2431)**

5'-GGTGBCBTTGBGCBTGTCGGCGC-3' **(FRAG. NO:2276) (SEQ. ID NO:2289)**
5'-GGTCCCGTTBBGBGTGGGCCC-3' **(FRAG. NO:2277) (SEQ. ID NO:2290)**
5'-GCCAGCCCAGCCACTCCACTTGGGGGC-3' **(FRAG. NO:2278) (SEQ. ID NO:2291)**
5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' **(FRAG. NO:2279) (SEQ. ID NO:2292)**
5'-GGCCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3'**(FRAG.NO:2280)(SEQ.ID NO:2293)**
5'-GGAGATAATGGCATTCACCACGCGGC-3' **(FRAG. NO:2281) (SEQ. ID NO:2294)**
5'-GGCCCAGCGCACGCCGCGCATCCGGCCC-3' **(FRAG. NO:2282) (SEQ. ID NO:2295)**
5'-GGGTTCTGACCTGCAGCCCCC-3' **(FRAG. NO:2283) (SEQ. ID NO:2296)**
5'-GTCTCCTTGGCATTCCTGGGCCC-3' **(FRAG. NO:2284) (SEQ. ID NO:2297)**
5'-CAGTCACTCCTCTCCCTGCCCCC-3' **(FRAG. NO:2285) (SEQ. ID NO:2298)**
5'-CTTGCTGGGGCAGGGACGG-3' **(FRAG. NO:2286) (SEQ. ID NO:2299)**
5'-GGTGBCBTTGBGCBTGTCGGCGC-3' **(FRAG. NO:2287) (SEQ. ID NO:2300)**
5'-GGTCCCGTTBBGBGTGGGCCC-3' **(FRAG. NO:2288) (SEQ. ID NO:2301)**
5'-GCCAGCCCAGCCACTCCACTTGGGGGC-3' **(FRAG. NO:2289) (SEQ. ID NO:2302)**
5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' **(FRAG. NO:2290) (SEQ. ID NO:2303)**
5'-GGCCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3'**(FRAG.NO:2291)(SEQ.ID NO:2304)**
5'-GGAGATAATGGCATTCACCACGCGGC-3' **(FRAG. NO:2292) (SEQ. ID NO:2305)**
5'-GGCCCAGCGCACGCCGCGCATCCGGCCC-3' **(FRAG. NO:2293) (SEQ. ID NO:2306)**
5'-GGGTTCTGACCTGCAGCCCCC-3' **(FRAG. NO:2294) (SEQ. ID NO:2307)**
5'-GTCTCCTTGGCATTCCTGGGCCC-3' **(FRAG. NO:2295) (SEQ. ID NO:2308)**
5'-CAGTCACTCCTCTCCCTGCCCCC-3' **(FRAG. NO:2296) (SEQ. ID NO:2309)**
5'-CTTGCTGGGGCAGGGACGG-3' **(FRAG. NO:2297) (SEQ. ID NO:2310)**
5'-CCGTGTTGTCBGTGGTGCTG-3' **(FRAG. NO:2298) (SEQ. ID NO:2311)**
5'-CCCGTTTGBGGTBTGGC-3' **(FRAG. NO:2299) (SEQ. ID NO:2312)**
5'-GCTCCBCCBBTTCCCTTTTCTCC-3' **(FRAG. NO:2300) (SEQ. ID NO:2313)**
5'-TTGTTTTCCGTTTCTCTTG-3' **(FRAG. NO:2301) (SEQ. ID NO:2314)**
5'-CCGTCTGTGGTT-3' **(FRAG. NO:2302) (SEQ. ID NO:2315)**

<u>β2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'- GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA AGAGCAAGGC CACCGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC GAGCCCAGCA TCCGCAGTGT CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC CTGCTCTTCC GAGACTTCTG CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA TCAAGAAGTA CGACAAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTTGTCAA AACCTCCGAG GGGACGTGTT CCACAAATTC ATTGAGAGCG ATAAGTTCAC ACGGTTTTGC CAGTGGAAGA ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCGC ATCATTGGGC GCGGGGGCTT TGGCGAGGTC TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGTACGCCA TGAAGTGCCT GGACAAAAAG CGCATCAAGA TGAAGCAGGG GGAGGACCCTG GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC TGCATGTCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC GGTGGGGACC TGCACTACCA CCTCTCCCAG CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG CCGAGATCAT CCTGGGCCTG GAGCACATGC ACAACCGCTT CGTGGTCTAC CGGGACCTGA AGCCAGCCAA CATCCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC CTGGGCCTGG CCTGTGACTT CTCCAAGAAG AAGCCCCATG CCACCGTGGG CACCCACGGG TACATGGCTC CGGAGGTCCT GCAGAAGGGC GTGGCCTACG ACAGCAGTGC CGACTGGTTC TCTCTGGGGT GCATGCTCTT CAAGTTGCTG CGGGGGCACA GCCCCTTCCG GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCCGAC TCCTTCTCCC CTGAACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT CTTGCAGAAG TACCCTCCCC CGCTGATCCC CCCACGAGGG GAGGTGAACG CGGCCGACGC CTTCGACATT GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT

TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCCGCAGA GCCTGCTGAC CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC GGTGGGAAAC AGTTCATTTT GCAGTGCGAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG ACGCCTACCG CGACGCCCAG CAGCTGGTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA AGGTACACAG AAGGGCTTCC AGGCCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGGTCCAAG TCCTCCAAGA TCTTGACTTG CAGATTAAGG AGTTTGTTCA CCTAATCTGC TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCCTCTAGGT CTCTCCTCTC AGTAGCCCCA GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT TGGGAAAAGC ATCCCTGGTC AGGGCCTGCA TCAGGGCAGT GGCTGGCCAT GAGGACCCTG AGAAGTAGAC AGATTCACGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC ATGGGTATAT GGGTGGCGAG TGACTCACCA CCCACTGAGA GGAGAACCTC ACAAGCTCTG ACATGCTCTG GTTCCAGGTT CTGTTGGGGC TGATCCAAGA TGGTAGCCTA GAGGTGCACA GAGATGGGGG CCTTGCTTTG CAAAAGGATG CTGGCTGCTG GCCCACAGCA TGGTAATGAG ATTTGAGCTT TATGTGCCCA GGGCTGGGAG GAGGGTCCTG TCACTTTGAA AGCAAAGAGA GGCTCTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCTT GAGACACCTG GCTTTCCCCA CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCCGGCTG GGAGAGTTTT TACCGTAACT ACATGTGGAA CCATCCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGCT GGCCAGGGAC CTGGGTCTAT GAGCTGGTTG GGGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CCTTCTGCGG CCAGGATTGG TTCTAGAGTA GGAGGGGTGG GATCGGGGAT GGGGGAAGCC TGTAACTGCG CTGCAGTTGT CAGGTCCCAG GTTCTGGGTG ACCTACTAAG GATTCTGGGT CCAGTGTGGG TCCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG ACAGTGATCT GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCCAA GTCTAGAGTT CAGGGTCATG GTAGTAGCCT AGGCTCAGAA TCAAGGTTGG GGTCAGTAAC CAGGATGGGA TCGAGGTCAT GGTCCAAAAT CTGGATCTGG GGACCTGTTG GGGGTCTGAG GTGAGTGTCG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG CTGTGATCTG AGGTCATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG TCTGGTGTCA GGTCGTGGAC TGCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAAA GTCCCAGATG GTGTTCAGAG GTCTGAATCT GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG ATCACGTTTG GTGTCAGGGC TGCCGCCCGA CTGGGGAGCC TGGGATCCAG AGATGTGACC CGAGGTTGTG GTCAGAGAAT GGGTCTCGGG TCGTCTTCGT GCCGGGTCCC TGTCGTGTTC CAGGCCCGGG TCTCCGTCCA GCATCGAGGG CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCGCAGGTC TGGTTCGGGG TCAGATTCCG CGCGGCCTCC AGGGGGCGCC GTCGCCGCCC GGCTCGGCCC CTCGCGGGCT CGCTGGCGTT GTGCGCGGCA GGCGGGGCCG GAGGCGGCGG CGGCTCCGGG GGCGCGGGCC GGGCGGCGGC GGCGGCGGCG CCCCGACTGC AGTCCCGGCG GGAGCGGAGC GCGAAGCGCG GGGCCGGGCC CGGAGCCGGC GCCATGGGGC GGCGCCGCCT GTGAGCGGCG GCGAGCGGAG CCGCGGGCGC CGAGCAGGGC CAGGCGGGAG CGTCGGCGCC CGAGGCCGAG CGAGCCGCGG CCGGGCCGGG CCGAGCGCCG AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG CGGCGGGAGG AGGCAGCGCC GCCGCCAAGA TGGCGGACCT GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' **(FRAG. NO:_) (SEQ. ID NO:2430)**

5'-CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA AGGTACACAG AAGGGCTTCC AGGCCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGGTCCAAG TCCTCCAAGA TCTTGACTTG CAGATTAAGG AGTTTGTTCA CCTAATCTGC TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCCTCTAGGT CTCTCCTCTC AGTAGCCCCA GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT TGGGAAAAGC ATCCCTGGTC AGGGCCTGCA TCAGGGCAGT GGCTGGCCAT GAGGACCCTG AGAAGTAGAC AGATTCACGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC ATGGGTATAT GGGTGGCGAG TGACTCACCA CCCACTGAGA GGAGAACCTC ACAAGCTCTG ACATGCTCTG GTTCCAGGTT CTGTTGGGGC TGATCCAAGA TGGTAGCCTA GAGGTGCACA GAGATGGGGG CCTTGCTTTG CAAAAGGATG CTGGCTGCTG GCCCACAGCA TGGTAATGAG ATTTGAGCTT TATGTGCCCA GGGCTGGGAG GAGGGTCCTG TCACTTTGAA AGCAAAGAGA GGCTCTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCTT GAGACACCTG GCTTTCCCCA CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCCGGCTG GGAGAGTTTT TACCGTAACT ACATGTGGAA CCATCCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGCT GGCCAGGGAC CTGGGTCTAT GAGCTGGTTG GGGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CCTTCTGCGG CCAGGATTGG TTCTAGAGTA GGAGGGGTGG GATCGGGGAT GGGGGAAGCC TGTAACTGCG CTGCAGTTGT CAGGTCCCAG GTTCTGGGTG ACCTACTAAG GATTCTGGGT

CCAGTGTGGG TCCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG
ACAGTGATCT GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCCAA GTCTAGAGTT CAGGGTCATG
GTAGTAGCCT AGGGTCAGAA TCAAGGTTGG GGTCAGTAAC CAGGATGGGA TCGAGGTCAT GGTCCAAAAT
CTGGATCTGG GGACCTGTTG GGGGTCTGAG GTGAGTGTCG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG
CTGTGATCTG AGGTCATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG
TCTGGTGTCA GGTCGTGGAC TGCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAAA
GTCCCAGATG GTGTTCAGAG GTCTGAATCT GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG ATCACGTTTG
GTGTCAGGGC TGCCGCCCGA CTGGGGAGCC TGGGATCCAG AGATGTGACC CGAGGTTGTG GTCAGAGAAT
GGGTCTCGGG TCGTCTTCGT GCCGGGTCCC TGTCGTGTTC CAGGCCCGGG TCTCCGTCCA GCATCGAGGG
CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCGCAGGTC TGGTTCGGGG TCAGATTCCG CGCGGCCTCC
AGGGGGCGCC GTCGCCGCCC GGCTCGGCCC CTCGCGGGCT CGCTGGCGTT GTGCGCGGCA GGCGGGGCCG
GAGGCGGCGG CGGCTCCGGG GGCGCGGGCC GGGCGGCGGC GGCGGCGGCG CCCCGACTGC AGTCCCGGCG
GGAGCGGAGC GCGAAGCGCG GGGCCGGGCC CGGAGCCGGC GCCATGGGGC GGCGCCGCCT GTGAGCGGCG
GCGAGCGGAG CCGCGGGCGC CGAGCAGGGC CAGGCGGGAG CGTCGGCGCC CGAGGCCGAG CGAGCCGCGG
CCGGGCCGGG CCGAGCGCCG AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG CGGCGGGAGG AGGCAGCGCC
GCCGCCAAGA TGGCGGACCT GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA
AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' **(FRAG. NO:_) (SEQ. ID NO:2429)**

5'-GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
AGAGCAAGGC CACGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC GAGCCCAGCA TCCGCAGTGT
CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC
CTGCTCTTCC GAGACTTCTG CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA
TCAAGAAGTA CGAGAAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA
CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC
CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTTGTCAA AACCTCCGAG
GGGACGTGTT CCACAAATTC ATTGAGAGCG ATAAGTTCAC ACGGTTTTGC CAGTGGAAGA ATGTGGAGCT
CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCGC ATCATTGGGC GCGGGGGCTT TGGCGAGGTC
TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGTACGCCA TGAAGTGCCT GGACAAAAAG CGCATCAAGA
TGAAGCAGGG GGAGACCCTG GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC
ATTCATTGTC TGCATGTCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC
GGTGGGGACC TGCACTACCA CCTCTCCCAG CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG
CCGAGATCAT CCTGGGCCTG GAGCACATGC ACAACCGCTT CGTGGTCTAC CGGGACCTGA AGCCAGCCAA
CATCCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC CTGGGCCTGG CCTGTGACTT CTCCAAGAAG
AAGCCCCATG CCACCGTGGG CACCCACGGG TACATGGCTC CGGAGGTCCT GCAGAAGGGC GTGGCCTACG
ACAGCAGTGC CGACTGGTTC TCTCTGGGGT GCATGCTCTT CAAGTTGCTG CGGGGGCACA GCCCCTTCCG
GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCCGAC
TCCTTCTCCC CTGAACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT
GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT
CTTGCAGAAG TACCCTCCCC CGCTGATCCC CCCACGAGGG GAGGTGAACG CGGCCGACGC CTTCGACATT
GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT
TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA
GACAGACCGG CTGCAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG
GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCCGCAGA GCCTGCTGAC
CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC
GGTGGGAAAC AGTTCATTTT GCAGTGCGAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG
ACGCCTACCG CGACGCCCAG CAGCTGGTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT
GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT-3'
(FRAG. NO:_) (SEQ. ID NO:2428)

CCR-2 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT
GATGGATTAT ACACTTGACC TCAGTGTGAC AACAGTGACC GACTACTACT ACCCTGATAT CTTCTCAAGC
CCCTGTGATG CGGAACTTAT TCAGACAAAT GGCAAGTTGC TCCTTGCTGT CTTTTATTGC CTCCTGTTTG
TATTCAGTCT TCTGGGAAAC AGCCTGGTCA TCCTGGTCCT TGTGGTCTGC AAGAAGCTGA GGAGCATCAC
AGATGTATAC CTCTTGAACC TGGCCCTGTC TGACCTGCTT TTTGTCTTCT CCTTCCCCTT TCAGACCTAC
TATCTGCTGG ACCAGTGGGT GTTTGGGACT GTAATGTGCA AAGTGGTGTC TGGCTTTTAT TACATTGGCT
TCTACAGCAG CATGTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG GCTGTTGTCC ATGCCGTGTA
TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCCTGGCAG TATGGCTAAC CGCCATTATG
GCTACCATCC CATTGCTAGT GTTTTACCAA GTGGCCTCTG AAGATGGTGT TCTACAGTGT TATTCATTTT
ACAATCAACA GACTTTGAAG TGGAAGATCT TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTTGATCCC
ATTCACCATC TTTATGTTCT GCTACATTAA AATCCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG

ACCAAGGCCA TCAGGTTGGT GCTCATTGTG GTCATTGCAT CTTTACTTTT CTGGGTCCCA TTCAACGTGG TTCTTTTCCT CACTTCCTTG CACAGTATGC ACATCTTGGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA TGCCACCCAT GTCACAGAAA TCATTTCCTT TACTCACTGC TGTGTGAACC CTGTTATCTA TGCTTTTGTT GGGGAGAAGT TCAAGAAACA CCTCTCAGAA ATATTTCAGA AAAGTTGCAG CCAAATCTTC AACTACCTAG GAAGACAAAT GCCTAGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCCTCCC GTTCCTCCAG CGTAGACTAC ATTTTGTGAG GATCAATGAA GACTAAATAT AAAAAACATT TTCTTGAATG GCATGCTAGT AGCAGTGAGC AAAGGTGTGG GTGTGAAAGG TTTCCAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT GTTGCCAACA CTTGGAACAC AATGACTGGA GACATAGTTG TGCATGCCTG GCACAACATC AAGCCTGTGA TTGTGTTTAT TGATGATGTT GAACAAGTGG TGGCTTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAAGA TGTCTCCGGA ATTCGACAGG TTATCA-3' **(FRAG. NO:_) (SEQ. ID NO:2462)**

<u>CCR-4 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-TTTCATCTCT CCCGGCTTAT TTGCTGGTTT CTCCGAATGC GGGCCTTGTC TGGTTCACGC TGGATCCCCA ACGCCTAGAA CAGTGCGTGG CACGCAGTTC GTCCTTCTAT AAATATCGGA CTAAATGCAT CTCTGTGATG GTAATACCCA CACCGTGTTG TGAGAATGAA TGAGTGATTC TGTGCAAGTT CCTAGTGATC TGTTACAAAA AGTACTGGTC GCTAAATTAC TCTTATAATA AAGCATACTT TTAGGATAAT AAAGCACTAT TCGCGAATTG GTTACCGCTA TTATGAAATT ACTGAGCAAT ACATATCTAC ATCTGATCAG TCTCCAGAAT TATGCCAAAT CCTACCTTCT TCTGAAAGTA TCTCCTAATT ATCTGCACCT GACCCTAGTG ATGCTGTGAA TGTGCAAGTA TAGCTACATC CTCCGAAGGA AGGATCTTTA CTCCTTTTAC CTCCTGAATG GGCTGCGTCT GCTGAAAGCG CGGGGGAATG GGCGGTTGGA AGCTTGGCCC TACTTCCAGC ATTGCCGCCT ACTGGTTGGG TTACTCCAGC AAGTCACTCC CCTTCCCTGG GCCTCAGTGT CTCTACTGTA GCATTCCCAG GTCTGGAATT CCATCCACTT TAGCAAGGAT GGACGCGCCA CAGAGAGACG CGTTCCTAGC CCGCGCTTCC CACCTGTCTT CAGGCGCATC CCGCTTCCCT CAAACTTAGG AAATGCCTCT GGGAGGTCCT GTCCGGCTCC GGACTCACTA CCGACCACCC GCAAACAGCA GGGTCCCCTG GGCTTCCCAA GCCGCGCACC TCTCCGCCCC GCCCCTGCGC CCTCCTTCCT CGCGTCTGCC CCTCTCCCCC ACCCCGCCTT CTCCCTCCCC GCCCCAGCGG CGCATGCGCC GCGCTCGGAG CGTGTTTTTA TAAAAGTCCG GCCGCGGCCA GAAACTTCAG TTTGTTGGCT GCGGCAGCAG GTAGCAAAGT GACGCCGAGG GCCTGAGTGC TCCAGTAGCC ACCGCATCTG GAGAACCAGC GGTTACCATG GAGGGGATCA GTGTAAGTCC AGTTTCAACC TGCTTTGTCA TAAATGTACA AACGTTTGAA CTTAGAGCGC AGCCCCTCTC CGAGCGGGCA GAAGCGGCCA GGACATTGGA GGTACCCGTA CTCCAAAAAA GGGTCACCGA AAGGAGTTTT CTTGACCATG CCTATATAGT GCGGGTGGGT GGGGGGGGAG CAGGATTGGA ATCTTTTTCT CTGTGAGTCG AGGAGAAACG ACTGGAAAGA GCGTTCCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC CGCGCGCGGC GGCTTGCACG CTGTTTGCAA ACGTAAGAAC ATTCTGTGCA CAAGTGCAGA GAAGGCGTGC GCGCTGCCTC GGGACTCAGA CCACCGGTCT CTTCCTTGGG GAAGCGGGGA TGTCTTGGAG CGAGTTACAT TGTCTGAATT TAGAGGCGGA GGGCGGCGTG CCTGGGCTGA CTTCCCAGGA GGAGATTGCG CCCGCTTTAA CTTCGGGGTT AAGCGCCTGG TGACTGTTCT TGACACTGGG TGCGTGTTTG TTAAACTCTG TGCGGCCGAC GGAGCTGTGC CAGTCTCCCA GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA TCGAGTGGTG GCACCAGCTA GGAGTTGATC CGCCCGCGCG CTTTGGGTTT GAGGGGGAAA CCTTCCCGCC GTCCGAAGCG CGCCTCTTCC CCACGGCCGC GAGTGGGTCC TGCAGTTCGA GAGTTTGGGG TCGTGCAGAG GTCAGCGGAG TGGTTTGACC TCCCCTTTGA CACCGCGCAG CTGCCAGCCC TGAGATTTGC GCTCCGGGGA TAGGAGCGGG TACCGGGTGA GGGGCGGGGG CGGTTAAGAC CGCACCTGGG CTGCCAGGTC GCCGCCGCGA AGACTGGCAG GTGCAAGTGG GGAAACCGTT TGGCTCTCTC CGAGTCCAGT TGTGATGTTT AACCGTCGGT GGTTTCCAGA AACCTTTTGA AACCCTCTTG CTAGGGAGTT TTTGGTTTCC TGCAGCGGCG CGCAATTCAA AGACGCTCGC GGCCGAGCCG CCCAGTCGCT CCCCAGCACC CTGTGGGACA GAGCCTGGCG TGTCGCCCAG CGGAGCCCCT GCACCGCTGC TTGCGGGCGG TTGGCGTGGG TGTAGTGGGC AGCCGCGGCG GCCCGGGGCT GGACGACCCG GCCCCCCGCG TGCCCACCGC CTGGAGGCTT CCAGCTGCCC ACCTCCGGCC GGGTTAACTG GATCAGTGGC GGGGTAATGG GAAGCCACCC GGGAGAGTGA GGAAATGAAA CTTGGGGCGA GGACCACGGG TGCAGACCCC GTTACCTTCT CCACCCAGGA AAATGCCCCG CTCCCTAACG TCCCAAACGC GCCAAGTGAT AAACACGAGG ATGGCAAGAG ACCCACACAC CGGAGGAGCG CCCGCTTGGG GGAGGAGGTG CCGTTTGTTC ATTTTCTGAC ACTCCCGCCC AATATACCCC AAGCACCGAA GGGCCTTCGT TTTAAGACCG CATTCTCTTT ACCCACTACA AGTTGCTTGA AGCCCAGAAT GGTTTGTATT TAGGCAGGCG TGGGAAAATT AAGTTTTTGC GCTTTAGGAG AATGAGTCTT TGCAACGCCC CCGCCCTCCC CCCGTGATCC TCCCTTCTCC CCTCTTCCCT CCCTGGGCGA AAAACTTCTT ACAAAAAGTT AATCACTGCC CCTCCTAGCA GCACCCACCC CACCCCCCAC GCCGCCTGGG AGTGGCCTCT TTGTGTGTAT TTTTTTTTTC CTCCTAAGGA AGGTTTTTTT TCTTCCCTCT AGTGGGCGGG GCAGAGGAGT TAGCCAAGAT GTGACTTTGA AACCCTCAGC GTCTCAGTGC CCTTTTGTTC TAAACAAAGA ATTTTGTAAT TGGTTCTACC AAAGAAGGAT ATAATGAAGT CACTATGGGA AAAGATGGGG AGGAGAGTTG TAGGATTCTA CATTAATTCT CTTGTGCCCT TAGCCCACTA CTTCAGAATT TCCTGAAGAA AGCAAGCCTG AATTGGTTTT TTAAATTGCT TTAAAAATTT TTTTTAACTG GGTTAATGCT TGCTGAATTG GAAGTGAATG TCCATTCCTT TGCCTCTTTT GCAGATATAC ACTTCAGATA ACTACACCGA GGAAATGGGC TCAGGGGACT ATGACTCCAT GAAGGAACCC TGTTTCCGTG AAGAAAATGC TAATTTCAAT AAAATCTTCC TGCCCACCAT CTACTCCATC ATCTTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGGG TTACCAGAAG AAACTGAGAA GCATGACGGA CAAGTACAGG CTGCACCTGT CAGTGGCCGA CCTCCTCTTT GTCATCACGC TTCCCTTCTG GGCAGTTGAT GCCGTGGCAA ACTGGTACTT TGGGAACTTC CTATGCAAGG

CAGTCCATGT CATCTACACA GTCAACCTCT ACAGCAGTGT CCTCATCCTG GCCTTCATCA GTCTGGACCG
CTACCTGGCC ATCGTCCACG CCACCAACAG TCAGAGGCCA AGGAAGCTGT TGGCTGAAAA GGTGGTCTAT
GTTGGCGTCT GGATCCCTGC CCTCCTGCTG ACTATTCCCG ACTTCATCTT TGCCAACGTC AGTGAGGCAG
ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGTT GTGTTCCAGT TTCAGCACAT
CATGGTTGGC CTTATCCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC CAAGCTGTCA
CACTCCAAGG GCCACCAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCCT CATCCTGGCT TTCTTCGCCT
GTTGGCTGCC TTACTACATT GGGATCAGCA TCGACTCCTT CATCCTCCTG GAAATCATCA AGCAAGGGTG
TGAGTTTGAG AACACTGTGC ACAAGTGGAT TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTTGTCTG
AACCCCATCC TCTATGCTTT CCTTGGAGCC AAATTTAAAA CCTCTGCCCA GCACGCACTC ACCTCTGTGA
GCAGAGGGTC CAGCCTCAAG ATCCTCTCCA AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC
TGAGTCTTCA AGTTTTCACT CCAGCTAACA CAGATGTAAA AGACTTTTTT TTATACGATA AATAACTTTT
TTTTAAGTTA CACATTTTTC AGATATAAAA GACTGACCAA TATTGTACAG TTTTTATTGC TTGTTGGATT
TTTGTCTTGT GTTTCTTTAG TTTTTGTGAA GTTTAATTGA CTTATTTATA TAAATTTTTT TTGTTTCATA
TTGATGTGTG TCTAGGCAGG ACCTGTGGCC AAGTTCTTAG TTGCTGTATG TCTCGTGGTA GGACTGTAGA
AAAGGGAACT GAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG
CATAGATAAT CTCTCCATTC CCGTGGAACG TTTTTCCTGT TCTTAAGACG TGATTTTGCT GTAGAAGATG
GCACTTATAA CCAAAGCCCA AAGTGGTATA GAAATGCTGG TTTTTCAGTT TTCAGGAGTG GGTTGATTTC
AGCACCTACA GTGTACAGTC TTGTATTAAG TTGTTAATAA AAGTACATGT TAAACTTACT TAGTGTTATG
TTCTGATTTC TGTTGACATT CTTTTGGCTA GTAGAAGACA AAAGTAATAC ATTTATGGTA TGCAAAGCAC
TATCCTAGGT ATTTCATTGT AATATTTTAC TTACCCCTTA TCACAACTCT GATAGATTCT GCTTCTGTTA
CTAATTACAT TTTATAGAAG AGGAAACGGA GGCACAGAAA GCCTAAGTAA CTTGGTTAAA GGCATGTAGT
AAGTATCAAA TCCTGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT
TCAAATGGAA GTTTAGAAAT GGCCAGCCAG CACCTATTTG TATGAAAGGT CATCTTTCAG AGGATAAGCA
TGTATAAAGA AGAAAAGGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT C-3' (FRAG. NO:_) (SEQ. ID NO: 2463)

CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA
AAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA
AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA
CACACAGCAC AGGATCTGGT GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAC
GAAATGCTCA CACTTCTAAA CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA
CTTAAAAATA AAGCAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT
GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG
GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC
GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC
CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC
ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG
CGGGGCTGGA CCGCGCTTTG CTTGCTGAGT TTGCTGC CCTTTTTTGG CCTCGACGGC GGCAACCCAG
CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG
CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC ACCCCTCTCC
CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT
AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC
CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA
GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTTCTACAA ATGTATCCTA CCAAGAAACT ACAACACCTA
GTACCCTTGG AAGTACCAGC CTGCACCCTG TGTCTCAACA TGGCAATGAG GCCACAACAA ACATCACAGA
AACGACAGTC AAATTCACAT CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAAACTC TTCTGTCCAG
TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCCAG CCAACGTTTC AACTCCAGAG ACAACCTTGA
AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC CACTAGCACT AGCCTTGCAA CATCTCCCAC
TAAACCCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTC AGGCATCAGA
GAAGTGAAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG
ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCCAGGT
ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA
GAAATTTCCA GCAAACTCCA ACTTATGAAA AAGCACCAAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT
TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG
AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCCTG ATGAATCGCC GCAGCTGGAG CCCCACAGGA
GAAAGGCTGG GCGAAGACCC TTATTACACG GAAAACGGTG GAGGCCAGGG CTATAGCTCA GGACCTGGGA
CCTCCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC
CTCCAGAAAC GGCCATTCAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG
CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT CTGACCACGT GCTACCCCCA TGCTGGAGGT
GACATCTCTT ACGCCCAACC CTTCCCCACT GCACACACCT CAGAGGCTGT TCTTGGGGCC CTACACCTTG
AGGAGGGGGC AGGTAAACTC CTGTCCTTTA CACATTCGGC TCCCTGGAGC CAGACTCTGG TCTTCTTTGG
GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT
CACACAGGAC CCCCTTCCCC TACCCCCTCC TCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC
TTTTCTAGGC TACAATTTTC TCCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT

ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTTGC
CTTGAACCAC TTCCCTCATC TCTCCTCCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT
AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTTGCA GAGTCCTGCA CAGTTTTCTG GCTGGAGCCT
AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC TAGTCTCTCT GGGGCCACAC AGAAACTCTT
TTTGGGCTCC TTTTTCTCCC TCTGGATCAA AGTAGGCAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT
CTCACCTGTA CTCTTCCGAA AAATCCTCTT CCTCTGAGGC TGGATCCTAG CCTTATCCTC TGATCTCCAT
GGCTTCCTCC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT TGCCTCAGTC CCCCAACAGA TGCTTTTCTG
TCTCTGCCTC CCTCACCCTG AGCCCCTTCC TTGCTCTGCA CCCCCATATG GTCATAGCCC AGATCAGCTC
CTAACCCTTA TCACCAGCTG CCTCTTCTGT GGGTGACCCA GGTCCTTGTT TGCTGTTGAT TTCTTTCCAG
AGGGGTTGAG CAGGGATCCT GGTTTCAATG ACGGTTGGAA ATAGAAATTT CCAGAGAAGA GAGTATTGGG
TAGATATTTT TTCTGAATAC AAAGTGATGT GTTTAAATAC TGCAATTAAA GTGATACTGA AACAC-3' **(FRAG.No:_)**
(SEQ. ID NO:2466)

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA
AAAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA
AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA
CACACAGCAC AGGATCTGGT GAGGCTATCA CTAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAC
GAAATGCTCA CACTTCTAAA CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA
CTTAAAAATA AAGCAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT
GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG
GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC
GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC
CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC
ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG
CGGGGCTGGA CCGCGCTTTG CTTGCTGAGT TTGCTGC-3' **(FRAG. NO:_) (SEQ. ID NO:2464)**

5'-CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG
GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG
GAAAAAAGCA AGAATCCCCC ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG
AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC
GCGAGGGCCC AGGATGCCGC GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTCATG
AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTTCTACAA
ATGTATCCTA CCAAGAAACT ACAACACCTA GTACCCTTGG AAGTACCAGC CTGCACCCTG TGTCTCAACA
TGGCAATGAG GCCACAACAA ACATCACAGA AACGACAGTC AAATTCACAT CTACCTCTGT GATAACCTCA
GTTTATGGAA ACACAAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCCAG
CCAACGTTTC AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC
CACTAGCACT AGCCTTGCAA CATCTCCCAC TAAACCCTAT ACATCATCTT CTCCTATCCT AAGTGACATC
AAGGCAGAAA TCAAATGTTC AGGCATCAGA GAAGTGAAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA
AGACCTCCAG CTGTGCGGAG TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA
GCAGGCTGAT GCTCATGCTG GGGCCCAGGT ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG
TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA GCAAACTCCA ACTTATGAAA AAGCACCAAT
CTGACCTGAA AAAGCTGGGG ATCCTAGATT TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA
AAAGACCCTG ATTGCACTGG TCACCTCGGG AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCCTG
ATGAATCGCC GCACCTGGAG CCCCACAGGA GAAAGGCTGG GCGAAGACCC TTATTACACG GAAAACGGTG
GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG
GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTCAG CAAGACAACA CGTGGTGGCT
GATACCGAAT TGTCACTCGG CTAGGTGGGG CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT
CTGACCACGT GCTACCCCCA TGCTGGAGGT GACATCTCTT ACGCCCAACC CTTCCCCACT GCACACACCT
CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAAACTC CTGTCCTTTA CACATTCGGC
TCCCTGGAGC CAGACTCTGG TCTTCTTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT
CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCCC TACCCCCTCC TCTCTGCCGC
AATACAGGAA CCCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTTC TCCCAGGAAG CTTTGATTTT
TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT
TGTAATGATA TAGCCAGAAA AACGTGTTGC CTTGAACCAC TTCCCTCATC TCTCCTCCAA GACACTGTGG
ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTTGCA
GAGTCCTGCA CAGTTTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC
TAGTCTCTCT GGGGCCACAC AGAAACTCTT TTTGGGCTCC TTTTTCTCCC TCTGGATCAA AGTAGGCAGG
ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTTCCGAA AAATCCTCTT CCTCTGAGGC
TGGATCCTAG CCTTATCCTC TGATCTCCAT GGCTTCCTCC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT
TGCCTCAGTC CCCCAACAGA TGCTTTTCTG TCTCTGCCTC CCTCACCCTG AGCCCCTTCC TTGCTCTGCA
CCCCCATATG GTCATAGCCC AGATCAGCTC CTAACCCTTA TCACCAGCTG CCTCTTCTGT GGGTGACCCA
GGTCCTTGTT TGCTGTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTTCAATG ACGGTTGGAA
ATAGAAATTT CCAGAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT GTTTAAATAC

TGCAATTAAA GTGATACTGA AACAC-3' **(FRAG. No:_) (SEQ. ID NO:2465)**

Eotaxin Antisense Nucleic Acids and Oligonucleotide Fragments

5'-GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAATAAAC CAGAAACCAC CACCTCTCAC
GCCAAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC TGTGGCTGCT GCTCATAGCA
GCTGCCTTCA GCCCCCAGGG GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTTT AACCTGGCCA
ATAGGAAGAT ACCCCTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC
TGTGATCTTC AAGACCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC
ATGAAGTATC TGGACCAAAA ATCTCCAACT CCAAAGCCAT AAATAATCAC CATTTTTGAA ACCAAACCAG
AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA
AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAAC GTATTGCATT TAATTTATTG
AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT AAACTGTAAA GCTTTGTGCA GATTCTTTAC
CCCCTGGGAG CCCCAATTCG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG
GAATCTTGTA AAGGTCCTGG CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG
ACTCATTAAA TGGAAGTAAA TGTTGTTTTA GGAATAC ATGAAGGTCT CCGCAGCACT TCTGTGGCTG
CTGCTCATAG CAGCTGCCTT CAGCCCCCAG GGGCTCGCTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT
TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG
TCCCCAGAAA GCTCTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG
GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGCC ATAA CCACATATTC CCCTCCTTTT
CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC CCTCCTACTA GCTTGCCTCT CTTCTGTTCT
GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA
AAGGCTTCCC TGGAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA
GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCACGCCA AAGCTCACAC CTTCAGCCTC CAACATGAAG
GTCTCCGCAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC CCAGGGGCTC GCTGGGCCAG
GTAAGCCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT ACTAGGTCAG CAAGAATCTT
TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA ACAGGTTTTG TGGGTGGACA AGAAATGCCT
CAACCGTCAC ATCCAGTCAC TGGAAGAGCC AGAACTAGAA AGCTCCCGAG TCTTTTCCCC ACATTCAAGA
GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGGAATGGCT CTGTCTTACT
GTGGGCATGG TGGCCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA TTAGAAGCTC AGTATGTTAA
TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGGAT CTCTTGAGGT
GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA ACTCATTTTC CCATACTCTG
GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG GTAACAAACA GTTCTAAATT
ATCAATGACT TAACAGAATT AACTAAATTA ACAAAAGTTA CTTTCTCACT TGTACTAAAT ATCTATAATG
TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG AAGTTGCCAT GTGGGGGAAC
ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAT AGGCAATGCA CTGTGGCTCA
AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAACTAATTA ATGCCTCCAA CCAAACAAAA
GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA ATATTTGGTG AAAATTACCA
TGACCATCAC ATGCCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG TCACATTGAC CAAGCTTTGT
CCATACACTC TACAGTAATG ATGAGTCCTC AGTGCACAGG GGAGGATGCT GAAGACACAG GACAGCATCC
TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCCTTGC TTTCTCCTAA
CTTCCTTTAC AAACTCATGC TTGGAAATGT CTATGTATCA TCATGTGGCT CATTTTTTTC TCTGTTCATT
TTTTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT GGCCAATAGG AAGATACCCC
TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG AAAGCTGTGA TGTAAGTAAA
TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG GCACAGAGTC AAGAACTGTG GGAGTCATAG
ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT
GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTTAC TGGGCCTTTA
AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG
GTCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAATCCTT CCAATTGCAT CCTGATTCTC
CCCACAGCTT CAAGACCAAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG AAGAAGTGGG TGCAGGATTC
CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA CCATTTTTGA AACCAAACCA
GAGCCTGAGT GTTGCCTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG GTAACCTCAT TATCAGTCCA
AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA AAACGTATTG CATTTAATTT
ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG TAAAGCTTTG TGCAGATTCT
TTACCCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC TCTCTTCCTC
CCTGGAATCT TGTAAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA TTGTTCTTGT GAACCCAAAG
TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG TGCATATTTT ATTATAGTCA
CTAGTTGTAA TTTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' (FRAG.NO:_) (SEQ. ID NO:2494)

5'-GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAATAAAC CAGAAACCAC CACCTCTCAC
GCCAAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC TGTGGCTGCT GCTCATAGCA
GCTGCCTTCA GCCCCCAGGG GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTTT AACCTGGCCA

ATAGGAAGAT ACCCCTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC
TGTGATCTTC AAGACCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC
ATGAAGTATC TGGACCAAAA ATCTCCAACT CCAAAGCCAT AAATAATCAC CATTTTTGAA ACCAAACCAG
AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA
AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAAC GTATTGCATT TAATTTATTG
AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT AAACTGTAAA GCTTTGTGCA GATTCTTTAC
CCCCTGGGAG CCCCAATTCG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG
GAATCTTGTA AAGGTCCTGG CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG
ACTCATTAAA TGGAAGTAAA TGTTGTTTTA GGAATAC-3' **(FRAG.NO:_) (SEQ. ID NO:2491)**

5'-ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG GGGCTCGCTG
GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA
GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG
GATATCTGTG CCGACCCCAA GAAGAAGTGG GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA
CTCCAAAGCC ATAA-3' **(FRAG. NO:_) (SEQ. ID NO:2492)**

5'-CCACATATTC CCCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC CCTCCTACTA
GCTTGCCTCT CTTCTGTTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA
TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC
AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCACGCCA AAGCTCACAC
CTTCAGCCTC CAACATGAAG GTCTCCGCAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC
CCAGGGGCTC GCTCGGCCAG GTAAGCCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT
ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA ACAGGTTTTG
TGGGTGGACA AGAAATGCCT CAACCGTCAC ATCCAGTCAC TGGAAGAGCC AGAACTAGAA AGCTCCCGAG
TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTTGGGAATG
GGGAATGGCT CTGTCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA
TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT
CCCAGGGGAT CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA
ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG
GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA ACAAAAGTTA CTTTCTCACT
TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG
AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAT
AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAACTAATTA
ATGCCTCCAA CCAAACAAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA
ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG
TCACATTGAC CAACCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC AGTGCACAGG GGAGGATGCT
GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC
AATTCCTTGC TTTCTCCTAA CTTCCTTTAC AAAGTCATGC TTGGAAATGT CTATGTATCA TCATGTGGCT
CATTTTTTTC TCTGTTCATT TTTTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT
GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG
AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG GCACAGAGTC
AAGAACTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA
GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG
ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC
CCTTTGTCCA GGGGCAGATG GTCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAATCCTT
CCAATTGCAT CCTGATTCTC CCCACAGCTT CAAGACCAAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG
AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA
CCATTTTTGA AACCAAACCA GAGCCTGAGT GTTGCCTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG
GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA
AAACGTATTG CATTTAATTT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG
TAAAGCTTTG TGCAGATTCT TTACCCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT
CCCCCTCTCC TCTCTTCCTC CCTGGAATCT TGTAAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA
TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG
TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' **(FRAG.NO:_) (SEQ. ID NO:2493)**

FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments

5'- GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA
GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCCTGTGGG ACCGCTATGG
GCGTGGAGAT CGACACCATC TCCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA
GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG

AGATGGCTGC TGCTCACCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC
AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTCGTC
AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCATTTTG
TGTGATGCAT GTACTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT ACACTGCCTT
ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
CTTGAGCCAG TTACCTTTGC TGTCACTTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA GAATTCGGGC CGCCGCCAGG TCGCTGTTGG
TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAAACCA
TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGGATGCT
TGAAGATGGA AAGAAATTTG ATTCCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG
GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT
CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGGCAT CATCCCACCA CATGCCACTC TCGTCTTCGA
TGTGGAGCTT CTAAAACTGG AATGACAGGA ATGGCCTCCT CCCTTAGCTC CCTGTTCTTG GATCTGCCAT
GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC
TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC TCAGCTTTGC TTCCGACACC TCTGTTTCCT
CTTCCCCTTT CTCCTCGTAT GTGTGTTTAC CTAAACTATA TGCCATAAAC CTCAAGTTAT TCATTTTATT
TTGTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA GTACATGGTC
AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA
ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAA CATTCTTGCT GCTGCGCTGC
AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT
AAATTAAAAG CCCTACCTAA AACTGAGGTG GGGATGGGGA GAGCCTTTGC CTCCACCATT CCCACCCACC
CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC ACTGCAATGC TGGACACTAC AGGTATCTGT
CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCATCCTGT GGTTTTTCTA
ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT TCCTAAATCT TAAGAACTTT
AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCCAGCC ATCATGACAA
ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT
TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTTCCTCC CTCAGCCCCT TCTCACCCCT TTGCTGTCCT
GTGTAGTGAT TTGCTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT
TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG
GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG
AAAGAAATTT GATTCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC
CGAGGCTGGG AAGAAGGGGT TGCCCAGATG AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT
ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT
TCTAAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC
TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCCTGATG TTCCACTCCA CTTTGTATAG
ACATCTGCCC TGACTGAATG TGTTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT
TCTCCTCGTA TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' **(FRAG.NO:_) (SEQ. ID NO:2499)**

5'- GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA-3' **(FRAG. No:_)(SEQ. ID NO: 2495)**

5'-GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCCTGTGGG CCGCTATGG
GCGTGGAGAT CGACACCATC TCCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA
GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG
AGATGGCTGC TGCTCACCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC
AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTCGTC
AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCATTTTG
TGTGATGCAT GTACTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT ACACTGCCTT
ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
CTTGAGCCAG TTACCTTTGC TGTCACTTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA-3' **(FRAG. NO:_) (SEQ. ID NO:2496)**

5'-GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG
CCGCCGCCAT GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA
GACCTGCGTG GTGCACTACA CCGGGATGCT TGAAGATGGA AAGAAATTTG ATTCCTCCCG GGACAGAAAC
AAGCCCTTTA AGTTTATGCT AGGCAAGCAG GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA
GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGGCAT
CATCCCACCA CATGCCACTC TCGTCTTCGA TGTGGAGCTT CTAAAACTGG AATGACAGGA ATGGCCTCCT
CCCTTAGCTC CCTGTTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA
TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC
TCAGCTTTGC TTCCGACACC TCTGTTTCCT CTTCCCCTTT CTCCTCGTAT GTGTGTTTAC CTAAACTATA

TGCCATAAAC CTCAAGTTAT TCATTTTATT TTGTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAA CATTCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAAAG CCCTACCTAA AACTGAGGTG GGGATGGGGA GAGCCTTTGC CTCCACCATT CCCACCCACC CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC ACTGCAATGC TGGACACTAC AGGTATCTGT CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCACCCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTTCCTCC CTCAGCCCCT TCTCACCCCT TTGCTGTCCT GTGTAGTGAT TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC-3' **(FRAG.NO:_) (SEQ. ID NO:2497)**

5' GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTCCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCCAGATG AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT TCTAAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGACTGAATG TGTTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT TCTCCTCGTA TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' **(FRAG. NO:_) (SEQ. ID NO:2498)**

wherein B is adenosine, or, more preferably, replaces adenosine and is an "equivame\\lent" or a "universal" base, and adenosine A_{2a} receptor agonist or only minimally antagonist, an adenosine A_{2b} receptor antagonist, an adenosine A_3 receptor antagonist, or an adenosine A_1 receptor antagonist. Similarly, adenosine (A) may always be replaced by an "alternative", "equivalent" and/or "universal" base having a small fraction, preferably less than 0.3 of the activity of adenosine at the adenosine receptor(s), as described above.

In one preferred embodiment, the links between neighboring mononucleotides are phosphodiester links. In another preferred, at least one mononucleotide phosphodiester residue of the anti-sense oligonucleotide(s) is substituted by a methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, 2'-O-methyl, methylene(methyimino), methyleneoxy (methylimino), phosphoramidate residues, and combinations thereof. The oligos having one or more phosphodiester residues substituted by one or more of the other residues are generally longer lasting, given that these residues are more resistant to hydrolysis than the phosphodiester residue. In some cases up to about 10%, about 30%, about 50%, about 75%, and even all phosphodiester residues may be substituted (100%). Typically, the multiple target anti-sense oligonucleotide (oligo) of the invention comprises at least about 7 mononucleotides, in some instances up to 60 and more mononucleotides, preferably about 10 to about 36, and more preferably about 12 to about 21 mononucleotides. However, other lengths are also suitable depending on the length of the target macromolecule. Examples of the MTA oligos of the invention are provided in Table 3 below, which includes ninety-four sequences (SEQ ID NOS.: 2316 through 2410).

Table 3: MTA Oligos, Location Targeted & Target

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
HUMNFKBP65A AS				
CCC GGC CCC GCC TCG TGC C	3019	5'=1	EPI 2192	
CGT CCB TGC CGC GGG CCC	3020	5'=28 (AUG)	EPI 2193	
GCC CCG CTG CTT GGG CTG CTC TGC CGG G	3021	5'=65	EPI 2194	
TCT GTG CTC CTC TCG CCT GGG	3022	5'=137	EPI 2195	
TGG TGG GGT GGG TCT TGG TGG	3023	5'=159	EPI 2196	
CTG TCC CTG GTC CTG TG	3024	5'=196	EPI 2197	

GGT CCC GCT TCT TC	3025	5'=362	EPI 2198	
GGG GTT GTT GTT GGT CTG G	3026	5'=401	EPI 2199	
TGT CCT CTT TCT GC	3026	5'=656	EPI 2200	
GCC TCG GGC CTC CC	3027	5'=697	EPI 2201	
GGC TGG GGT CTG CGT	3028	5'=769	EPI 2202	
GGC CGG GGG TCG GTG GGT CCG CTG	3029	5'=953	EPI 2203	
GGG CTG GGG TGC TGG CTT GGG G	3030	5'=1022	EPI 2204	
GGG GCT GGG GCC TGG GCC	3031	5'=1208	EPI 2205	
GCC TGG GTG GGC TTG GGG GC	3032	5'=1272	EPI 2206	
GCT GGG TCT GTG CTG TTG CC	3033	5'=1362	EPI 2207	
GTT GTG TGG GGG GCC	3034	5'= 1451	EPI 2208	
GCT GGG TCG GGG GGC CTC TGG GCT GTC	3035	5'=1511	EPI 2209	
GCC CCG GGG CCC CC	3036	5'=1550	EPI 2210	
TGG CTC CCC CCT CC	3037	5'=1772	EPI 2211	
GCT CCC CCC TTT CC	3038	5'=1863	EPI 2212	
CGG ACG AAG ACA GAG A	3039	5'=1979	EPI 2213	
GGC TTT GTG GGC TC	3040	5'=2011	EPI 2214	
GCC TGC TCT CCC CC	3041	5'=2312	EPI 2215	
CCC GGC CCC GCC **BCG** **BBC** C	3042	intron	EPI 2192-01A	HSU50136C4Synth
CCC GGC CCC GCC BCG	3043	intron	EPI 2192-01B	
CCC GGC CCC GCC BCG BBC C	3044	5'untr	EPI 2192-02A	HUMLIPOX5LO
CCC GGC CCC GCC **BCG**	3045	5'untr	EPI 2192-02B	
CCC G**B**C CCC GCC TC**B** **B**G	3046	trans	EPI 2192-03A	HSNFKBS Subunit
CCC G**B**C CCC GCC TC	3047	trans	EPI 2192-03B	
CCG GCC CCG CCT C	3048	5'untr	EPI 2192-04	TGFβR1
CCC G**BB** CCC GC**B** T**B**G TGC C	3049	5'trans	EPI 2192-05A	HSU58198I1 enhan
CCC GC**B** T**B**G TGC C	3050	5'untr	EPI 2192-05B	
CCC GG**B** CCC **B**CC **BB**G TGC C	3051	3'trans	EPI 2192-06	HSVECAD
C**B**G **BB**C CCG CCT CGT GCC	3052	intron	EPI 2192-07A	NFKB2
C CCG CCT CGT GCC	3053	intron	EPI 2192-07B	NFKB2
CCG GC**B** CCG CCT C**B**T GCC	3054	5'trans	EPI 2192-08	Carboxypep
CCG GCC CCG CC**B** C**B**T GCC	3055	3'trans	EPI 2192-09	HumADRA2Cα2AdrKid
CCC G**B**C CCC G**B**C TCG	3056	5'untrs	EPI 2192-10	HUMFK506B
CCC GGC C**B**C G**B**C TCG	3057	5'untrs	EPI 2192-11	HSNBARKS1βAdrKin
CCC GGC CC**B** GCC T**B**G	3058	5'UTR	EPI 2192-12	HSNFXN1(NFKB1)
CCC GGC **B**C**B** G**B**C TCG T**B**C C	3059	3'UTR	EPI 2192-13	HSILF(transcrp. Factor ILF)
CCC GGC CCC GCC **B**CG	3060		EPI-2192-14	NFKB/C4Syn/5-LO/ TGFBrec1 MTA
CCC GGC CCC GCC **B**CG	3061		EPI-2192-15NFKB/C4Syn/5-LOMTA	
TCC **B**TG CCG CGG GC	3062	3' trans	EPI-2193-01	METOncogene
TCC **B**TG CC**B** CGG GCC	3063	3' trans	EPI-2193-02	HSFGR2(IG)
TCC **B**TG CC**B** CGG GCC	3064	mid cod	EPI-2193-03	5-LO
TCC **B**TG CC**B** C**B**G GCC	3065	mid cod	EPI-2193-04	HUMTK14
GTC C**B**T G**B**C GCG G	3066	3'trans	EPI-2193-05	HUMTNFR
TC C**B**T G**B**C GCG GG	3067	AUG		Probl.HUMPTCH cardiacK+channel
TCT G**B**G CTC CTC T**BB** CCT GGG	3068	intr	EPI-2195-01	humCSPAcytotox. Ser.Protease
CTG TGC **B**CC T**BB** C**B**C CTG GG	3069	intr	EPI-2195-02	HSINOSX08induc.NOS
TGT G**B**T CC**B** CT**B** G**B**C TGG G	3070		EPI-2195-03	HUMACHRM2musc.m2 acetylch.rec.
TCT GT**B** CTC **BB**C TC**B** CCT G	3071		EPI-2195-04	s86371s1 Neurokinin3Recept
TGC TCC TC**B** C**BB** CTG GG	3072		EPI-2195-05	HUMMIP1 Amacro inflam.factor

Table 3: MTA Oligos, Location Targeted & Target (Cont'd)

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
CTC CTC TBG CCT GG	3073		EPI-2195-06	HSNBARKS4 β-Adr Rec Kinase
GTG CTC CBB TCB BCT GGG	3074		EPI-2195-07	HSTNFR2SO6TNF R2
GTG CBC CBB TCB CCT GGG	3075		EPI-2195-08	humfkbp fk506 binding prot.
TCT GTG CBC CTC TBG BCT	3076	exon	EPI-2195-09	HSNBARKS1β-Adr. Recept.Kinase
CTG TBB TCC TBB CBC CTG G	3077	intron	EPI-2195-10	HUMIL8
TGT GCT BBT CBC BCB TGG G	3078		EPI-2195-11	HSU50157 PDE4
GTG CBC CBC TCB CCT G	3079	intron/exon	EPI-2195-12	IL-2 R
CTG TGC BCC TCT C	3080	3'UTR	EPI-2203-05	IL-6 R HSIL6R
CBG TGC BCC BCT CBC CTG	3081	intr/ex	EPI-2203-06A	HSIL2rG6
G TGC BCC BCT CBC CTG	3082	intr/ex	EPI-2203-06B	HSIL2rG6
CBC CTC TCB CCT GGG	3083	coding	EPI-2203-07A	HUMIL71
C CTC TCB CCT GCG	3084	coding	EPI-2203-07B	IL-7 HUMIL71
GCT CCB CTC GCC T	3085	coding	EPI-2203-08	IL-6 R HSI6REC
TGC TCC TCB CGC C	3086	intron PDGF A	EPI-2303-09	Chain HUMPDGFAB
GTT GTT GBT CTG G	3087	3'utr	EPI-2199-01	GATA-4Transcrip. Factor for IL-5
GGT TGB BBT TGG TCT TGG	3088	Coding	EPI-2199-02	TNFα HUMTNFA
GGT TGT TGB TGB TCT G	3089	Far 5'UTR	EPI-2199-03	HSSUBP1G(Sub Pr)
GGG TTB BBG TTG BTC TGG	3090	Coding	EPI-2199-04	NeutrophilAdh. R HUMNARIA
GGG TTB BBG TTG BTC TGG	3091	HSHM2	EPI-2199-05	m2 Muscarinic R
TTG TTG TBG BTC TGG	3092	HUML1CAM	EPI-2199-06	L1 LeukAadhProt
GGG TBG BBG BGT CCG CTG	3093	coding	EPI-2203-01	HUMGATA2A
GGG TCB GBG GBT CBG CTG	3094	S71424S2	EPI-2203-02	IGE eps
GGG TBG GTG GGT C	3095	coding	EPI-2203-03	HSGCSFR2
GGG TCG GBG GGT CBG C	3096	HUMITGF	EPI-2203-04	TGFβ3
GGG TGG GCT T	3097	HUMNK65PRO	EPI-2206-01	NFKB/NK & TCell Activating Prot
GGG TGG GCT TGG G	3098	HUMPEREEB	EPI 2206-02	NFKB/Prostagl. EP3 Rec
CCTGGGTGGGBBTGGG	3099		EPI 2206-03	HSNF2B/GCSF NFKB/GranuLocCSF/ Transcr.FactorNF2B
CCTGGBTGGGCBTGGG	3100		EPI-2206-04	HUMLAP/NFKB Leuk.Adhes.Prot
GCCTGBGTGBBCTTGGG	3101		EPI2206-05	NFKB/Endothel N2 S63833
CCCAVGVCCVCCCAGGC	3102		EPI 2206-06	NFKBAS13/B Lymph SerThrProt.Kinase
AGCCCACCCAGGC	3103		EPI2206-07	NFKBAS13/GCSF1 HSGCSFR1Rec
BCCTGGGTGGGCTB	3104		EPI2206-08	NFKBAS13/GCSF1/ NK7TCELLACT.Prot
GGTGGGCTTGGG	3105		EPI 2206-09	NFKBAS13/ HSTGFB1 TGFB
CCBBGGTGGGCTTGGG	3106		EPI 2206-10	NFKBAS13/ HSTGFB1 TGFB1
CTGGGTGGGBBTGGG	3107		EPI 2206-11	NFKBAS13/ HSGCSFR1 GCSFR1
CCBGGGTGGGCTTGG	3108		EPI 2206-12	NFKBAS13/HUMCD30A LymphActAntigCoding
GGGTGGGCTTGG	3109		EPI-2206-12B	NFKBAS13/HUMCD30A
CCTGBGTGBGCBTGGG	3110		EPI 2206-13	NFKBAS13/HUMCAM1V Vasc.Endoth.Cell Adh.Molec

B: Universal Base

The MTA oligos of Table 3 are suitable for use with two or more of the targets listed in Table 4 below.

Table 4: Targets for the MTA Oligos of Table 3

Compound	Target
EPI 2010	Adenosine A1 receptor
EPI 2045	Adenosine A3 receptor
EPI 2873, EPI 2193	NFκB
EPI 1873	Interleukin-1
EPI 1857	Interleukin -5
EPI 2945	Interleukin -4
EPI 2977	Interleukin -8
EPI 2031	5-Lipoxygenase
EPI 1898	Leukotriene C-4 Synthase
EPI 1856	Eotaxin
EPI 1131	ICAM
EPI 1085	VCAM
EPI 2085	TNFα
EPI 1908	PAF
EPI 1925	IL-4 receptor
EPI 2643	β2 aderenergic receptor kinase
EPI 2934	Tryptase
EPI 2033	Major Basic Protein
EPI 2795	Eosinophil Peroxidase

NfκB: nuclear factor κB
ICAM: intracellular adhesion molecule
VCAM: vascular cell adhesion molecule
TNF: tumor necrosis factor
PAF: platelet activating factor

The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein, whether for existing targets or those to be found in the future. Sequences for many target genes of different systems are presently known. See, GenBank data base, NIH, the entire sequences of which are incorporated here by reference. The sequences of those genes, whose sequences are not yet available, may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, anti-sense oligonucleotides are produced as described above and utilized to validate the target by in vivo administration and testing for a reduction of the production of the targeted protein in accordance with standard techniques, and of specific functions. As already described above, the anti-sense oligonucleotides may be of any suitable length, e.g., from about 7 to about 60 nucleotides in length, depending on the particular target being bound and the mode of delivery thereof. The anti-sense oligonucleotide preferably is directed to an mRNA region containing a junction between intron and exon or to regions vicinal to the junction. Where the anti-sense oligonucleotide is directed to an intron/exon junction, it may either entirely overlie the junction or may be sufficiently close to the junction to inhibit splicing out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g., with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, 10, 5, 3, or 2 nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon and, more generally, those that target the coding region of the target mRNA. When practicing the present invention, the anti-sense oligonucleotides administered may be related in origin to the species to which it is administered. When treating humans, human anti-sense may be used if desired. Anti-sense oligos to endogenous sequences from other species,

however, are also encompassed.

Pharmaceutical compositions comprising an anti-sense oligonucleotide as given above effective to reduce expression of an A_1 or A_3 adenosine receptor by passing through a cell membrane and binding specifically with mRNA encoding an A_1 or A_3 adenosine receptor in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are provided in a suitable pharmaceutically acceptable carrier, e.g., sterile pyrogen-free saline solution. The anti-sense oligonucleotides may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g., in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may also be coupled to a substance which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject to inhibit the activation of a target, such as the adenosine receptors, which subject is in need of such treatment for any of the reasons discussed herein. Furthermore, the pharmaceutical formulation may also contain chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular uptake pathways to increase cellular concentrations of oligonucleotides. Examples of macromolecules used in this manner include transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin. In the pharmaceutical formulation, the anti-sense compound may be contained within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar, so long as the anti-sense oligonucleotide is contained therein. Positively charged lipids such as N- [1-(2, 3 -dioleoyloxi) propyl] -N, N, N-trimethylammoniumethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known. See, e.g., U.S. Patent Nos. 4,880,635 to Janoff et al.; 4,906,477 to Kurono et al.; 4,911,928 to Wallach; 4,917,951 to Wallach; 4,920,016 to Allen et al.; 4,921,757 to Wheatley et al.; etc.

Subjects may be administered the active composition by any means which transports the anti-sense nucleotide composition to the lung. The anti-sense compounds are particularly disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by generating an aerosol comprised of respirable particles, the respirable particles comprised of the anti-sense compound, which particles the subject inhales. The respirable particles may be liquid or solid. The particles may optionally contain other therapeutic ingredients. Particles comprised of anti-sense compound for practicing the present invention should include particles of respirable size: that is, particles of a size sufficiently small to pass through the mouth and larynx upon inhalation and into the bronchi and alveoli of the lungs. In general particles ranging from about .5 to about 10 microns in size are respirable. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is preferably minimized. For nasal administration, a particle size in the range of 10-500 :m is preferred to ensure retention in the nasal cavity. Thus, particles of about 4, about 10, about 25, about 50 to about 75, about 100, about 250, about 500, and other specific ranges therewithin, are preferred. Others, however, are also contemplated within the confines of this invention.

Liquid pharmaceutical compositions of active compound for producing an aerosol can be prepared by combining the anti-sense compound with a suitable vehicle, such as sterile pyrogen free water. Other therapeutic compounds may optionally be included. Solid particulate compositions containing respirable dry particles of micronized anti-sense compound may be prepared by grinding dry anti-sense compound with a mortar and pestle, and then passing the micronized composition through a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprised of the anti-sense compound may optionally contain a dispersant which serves to facilitate the formation of an aerosol. A suitable dispersant is lactose, which may be blended with the anti-sense compound in any suitable ratio (e.g., a 1 to 1 ratio by weight). Again, other therapeutic compounds may also be included.

The dosage of the anti-sense compound administered will depend upon the disease being treated, the condition of the subject, the particular formulation, the route of administration, the timing of administration to a subject, etc. In general, intracellular concentrations of the oligonucleotide of from about

0.01, about 0.05, about 0.1, about 0.2, about 1 to about 5 μM, about 50 μM, about 100 μM or more, and more particularly about 0.2 to about 0.5 μM, are desired. For administration to a subject such as a human, a dosage of from about 0.01, about 0.1 or about 1 mg/Kg up to about 50, about 100, or about 150 mg/Kg and even higher doses are typically employed depending on the route of administration as is known in the art. Depending on the solubility of the particular formulation of active compound administered, the daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically (i.e., as a rescue treatment) or prophylactically. Aerosols of liquid particles comprising the anti-sense compound may be produced by any suitable means, such as with a nebulizer. See, e.g., U.S. Patent No. 4,501,729. Nebulizers are commercially available devices which transform solutions or suspensions of the active ingredient into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in nebulizers consist of the active ingredient in a liquid carrier, the active ingredient comprising up to 40% w/w of the formulation, but preferably less than 20% w/w. The carrier is typically water or a dilute aqueous alcoholic solution, preferably made isotonic with body fluids by the addition of, for example, sodium chloride. Optional additives include preservatives if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants.

In one preferred embodiment, the pharmaceutical composition comprises nucleic acid(s) which comprise the anti-sense oligo(s) described above and one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as a single, or as part of a multiple component, surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends of the anti-sense oligo(s). Aerosols of solid particles comprising the active compound may likewise be produced with any solid particulate medicament aerosol generator. Aerosol generators for administering solid particulate medicaments to a subject produce particles which are respirable, as explained above, and generate a volume of aerosol containing a predetermined metered dose of a medicament at a rate suitable for human administration. One illustrative type of solid particulate aerosol generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder (e.g., a metered dose thereof effective to carry out the treatments described herein) is contained in capsules or cartridges, typically made of gelatin or plastic, which are either pierced or opened in situ and the powder delivered by air drawn through the device upon inhalation or by means of a manually-operated pump. The powder employed in the insufflator consists either solely of the active ingredient or of a powder blend comprising the active ingredient, a suitable powder diluent, such as lactose, and an optional surfactant. The active ingredient typically comprises from 0.1 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically containing a suspension or

solution formulation of the active ingredient in a liquefied propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically from 10 to 150 :l, to produce a fine particle spray containing the active ingredient. Suitable propellants include certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane and mixtures thereof. The formulation may additionally contain one or more co-solvents, for example, ethanol, surfactants, such as oleic acid or sorbitan trioleate, antioxidants and suitable flavoring agents. The aerosol, whether formed from solid or liquid particles, may be produced by the aerosol generator for example at a rate of from about 10, about 30, about 70 to about 100, about 150, about 150 liters per minute, more preferably from about 30 to 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater amounts of medicament, however, may be administered more rapidly as is known in the art.

The relevant disclosures of all scientific publications and patent references cited in this patent are specifically intended to be incorporated herein by reference, particularly in reference to preparatory methods and technologies which are enabling of the invention. The following examples are provided to illustrate the present invention, and should not be construed as limiting thereon.

EXAMPLES

In the following examples, :M means micromolar, ml means milliliters, :m means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius, :g means micrograms, mg means milligrams, g means grams, kg means kilograms, M means molar, and h or hr. means hours.

Example 1: Design and Synthesis of Anti-sense Oligonucleotides

The design of anti-sense oligonucleotides against the A_1 and A_3 adenosine receptors may require the solution of the complex secondary structure of the target A_1 receptor mRNA and the target A_3 receptor mRNA. After generating this structure, anti-sense nucleotide are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments.

The mRNA secondary structure of the adenosine A_1 receptor was analyzed and used as described above. to design a phosphorothioate anti-sense oligonucleotide. The anti-sense oligonucleotide which was synthesized was designated $HAdA_1AS$ and had the following sequence: **5' -GAT GGA GGG CGG CAT GGC GGG-3' (SEQ ID NO:1).** As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdAlMM1 was synthesized with the following sequence: **5' -GTA GCA GGC GGG GAT GGG GGC-3' (SEQ ID NO:2).** Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine A_1 receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine A_3 receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA3AS1) synthesized had the following sequence: **5' -GTT GTT GGG CAT CTT GCC-3' (SEQ ID NO:3).** As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA3MM1) was synthesized, having the following sequence: **5' -GTA CTT GCG GAT CTA GGC-3' (SEQ ID NO:4).** A second phosphorothioate anti-sense oligonucleotide (HAdA3AS2) was also designed and synthesized, having the following sequence: **5' -GTG GGC CTA GCT CTC GCC-3' (SEQ ID NO:5).** Its control oligonucleotide (HAdA3MM2) had the sequence: **5' -GTC GGG GTA CCT GTC GGC-3' (SEQ ID NO:6).** Phosphorothioate oligonucleotides were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, MD).

Example 2: In Vivo Testing of Adenosine A_1

Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human A_1 receptor (**SEQ ID NO:1**) described above. was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the A_1 adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory.

HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0 :M HAdAlAS or HAdAlMM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdAlAS-treated, HAdAlMM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdAlAS but not HAdAlMM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdAlAS is a good candidate for an anti-asthma drug since it depletes intracellular mRNA for the adenosine A_1 receptor, which is involved in asthma.

__Example 3:__ **In Vivo Efficacy of Adenosine A_1 Receptor Anti-sense Oligos**

A fortuitous homology between the rabbit and human DNA sequences within the adenosine A_1 gene overlapping the initiation codon permitted the use of the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine A_1 receptor in a rabbit model. Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (D. farinae) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (Cdyn) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC50 were obtained for aerosolized adenosine. Anti-sense (HAdAlAS) or mismatched control (HAdAlMM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 :g (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 :g in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerset, PA), producing aerosol droplets 80% of which were smaller than 5 :m in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC50 values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC50 values obtained for these animals prior to exposure to oligonucleotide. Following a 1 week interval, animals were crossed

over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC50 values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 5 below.

Table 5: **Effect of Adenosine A_1 Receptor Anti-sense Oligo upon PC50 Values in Asthmatic Rabbits**

Mismatch Control		A_1 Receptor Anti-sense Oligo	
Pre Oligonucleotide	**Post Oligonucleotide**	**Pre Oligonucleotide**	**Post Oligonucleotide**
3.56 ± 1.02	5.16 ± 1.03	2.36 ± 0.68	>19.5 ± 0.34**

The results are presented as the mean (n=8) ± SEM.
The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.
**Significantly different from all other groups, p<0 01

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC50 values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A_1 receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresponsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

Example 4: **Specificity of A_1-adenosine Receptor Anti-sense Oligonucleotide**

At the conclusion of the cross-over experiment of Example 3 above, airway smooth muscle from all rabbits was quantitatively analyzed for adenosine A_1 receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine A_2 receptors, which should not have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmacol. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by reference, with slight modifications. Crude plasma membrane preparations were stored at 70EC until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. The binding of [^{3}H] DPCPX (A_1 receptor-specific) or [^{3}H] CGS-21680 (A_1 receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine A_1 anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in A_1 receptor number compared to controls, as assayed by specific binding of the A_1-specific antagonist DPCPX. There was no change in adenosine A_2 receptor number, as assayed by specific binding of the A_2 receptor-specific agonist 2- [p- (2-carboxyethyl)-phenethylamino] -5' - (N-ethylcarboxamido) adenosine (CGS-21680). This is illustrated in Table 6 below.

Table 6: **Specificity of Action of Adenosine A_1 Receptor Oligonucleotide Anti-sense**

	Mismatch Control Oligonucleotide	A_1 Anti-sense Oligonucleotide

A_1-Specific Binding	1105 ± 48**	293 ± 18
A_2-Specific Binding	302 ± 22	442 ± 171

The results are presented as the mean (n = 8) ± SEM.
The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test
**Significantly different from mismatch control, p<0.01.

The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above. eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

Example 5: **Anti-sense Oligos directed to other Target Nucleic Acids**

This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were porepared to adenosine receptor mRNAs exemplified by the adenosine A_1, A_{2b} and A_3 receptor mRNAs. Anti-sense Oligo I was disclosed above (**SEQ. ID NO:1**).Five additional anti-sense phosphorothioate oligos were designed asnd synthesized as indicated above.

1- Oligo II (**SEQ. ID NO: 7**) also targeted to the adenosine A_1 receptor, but to a different region than Oligo I.
2- Oligo V (**SEQ. ID NO: 10**) targeted to the adenosine A_{2b} receptor.
3- Oligos III (**SEQ. ID NO: 8**) and IV (**SEQ. ID NO: 9**) targeted to different regions of the adenosine A_3 receptor.
4- Oligo I-PD (**SEQ. ID NO: 1681**)(a phosphodiester oligo of the same sequence as Oligo I).

These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific for that species, unless the segment of the target mRNA of other species happens to contain a similar sequences. All anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

Example 6: **Design & Sequences of other Anti-sense Oligos**

Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected for this study to complement the data on Oligo I (**SEQ ID NO: 1**) provided in Examples 1 to 4 above. This oligo is anti-sense to one region of the adenosine A_1 receptor mRNA. The oligos tested are identified as anti-sense Oligos I (**SEQ ID NO: 1**) and II (**SEQ. ID No: 7**) targeted to a different region of the adenosine A_1 receptor mRNA, Oligo V (**SEQ. ID No:8**) targeted to the adenosine A_{2b} receptor mRNA, and anti-sense Oligos III and IV (**SEQ. ID NOS: 9 and 10**) targeted to two different regions of the adenosine A_3 receptor mRNA. The sixth oligo (Oligo I-PD) is a phosphodiester version of Oligo I (**SEQ. ID NO:1**). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

(I) **Anti-sense Oligo I**

The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A_1 adenosine receptor mRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence:5'-GAT GGA GGG CGG CAT GGC GGG-3'(**SEQ.ID NO:1**). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., Nature, 385:721 (1977), the relevant portions of which reference are incorporated in their entireties herein by reference.

(II) **Anti-sense Oligo II**

A phosphorothioate anti-sense oligo (**SEQ. ID NO:7**) was designed in accordance with the invention to target the rabbit adenosine A_1 receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: **5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7).**

(III) Anti-sense Oligo III

A phosphorothioate anti-sense oligo other than that provided in Example 1 above (**SEQ. ID NO:8**) was designed in accordance with the invention to target the anti-sense A_3 receptor mRNA region +3 to + 22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: **5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8).**

(IV) Anti-sense Oligo IV

Yet another phosphorothioate anti-sense oligo (**SEQ. ID NO:9**) was designed in accordance with the invention to target the adenosine A_3 receptor mRNA region + 386 to + 401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: **5'-GGC CCA GGG CCA GCC-3' (SEQ. ID NO:9)**

(V) Anti-sense Oligo V

A phosphorothioate anti-sense oligo (**SEQ. ID NO:10**) was designed in accordance with the invention to target the adenosine A_{2b} receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: **5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10).**

(VI) A_1 Mismatch Oligos

Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (**SEQ. ID NO: 1**) described in Example 5 above: A_1 MM2:**5'-GTA GGT GGC GGG CAA GGC GGG-3' (SEQ. ID NO:2421), and** A_1 MM3:**5'-GAT GGA GGC GGG CAT GGC GGG-3' (SEQ. ID NO:2422).** Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A_1 receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

(VII) Anti-sense Oligo A_1-PD (Oligo VI)

A phosphodiester anti-sense oligo **(Oligo VI; SEQ. ID NO:2420)** having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'- GAT GGA GGG CGG CAT GGC GGG-3' (**SEQ. ID NO:2420**).

III) Controls

Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

<u>Example 7</u>: Synthesis of Anti-sense Oligos

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucleotide II (**SEQ. ID NO:7**), anti-sense oligonucleotide III (**SEQ. ID NO: 8**) and anti-sense oligonucleotide IV (**SEQ. ID NO: 9**) were each synthesized and purified in this manner.

<u>Example 8</u>: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (D. *farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali,

S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant portions of which are incorporated in their entireties here by reference. Immunizations were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

DOSE-RESPONSE STUDIES

Example 9: Experimental Setup

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:m in diameter. Equal volumes of the aerosols were administered directly to the lungs *via* an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC_{50} Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC_{50} values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

Example 10: Crossover Experiments

For some experiments utilizing anti-sense oligo I (**SEQ ID NO: 1**) and a corresponding mismatch control oligonucleotide A1MM2, following a 2 week interval, the animals were crossed over, with those previously administered the mismatch control A_1MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A_1MM2 oligo. The number of animals per group was as follows. For mismatch A_1MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A_1MM3 n=4 (Control 2) and for A_1AS anti-sense oligo I, n=8. The A_1MM3 oligo-treated animals were analyzed separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (**SEQ. ID NO: 1**), no PC_{50} value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC_{50} values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo (**SEQ ID NO: 1**), or the A_1MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

Example 11: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (**SEQ. ID No:1**) in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in Example 19 below and in Table 1 of Nyce & Metzger, Nature 385: 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (**SEQ. IS NOS; 7, 8 and 9**).

Example 12: Specificity of Oligo I for Adenosine A_1 Receptor (Receptor Binding Studies)

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi from rabbits which had been administered 20 mg oligo I (**SEQ ID NO: 1**) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. See, Bradford, M. M. Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [^{3}H]DPCPX, [^{3}H]NPC17731, or [^{3}H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., Pharmacol. Exptl. Ther. 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

Example 13: Pulmonary Function Measurements (Compliance c_{DYN} and Resistance)

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, Proc. Soc. Exp. Biol. Med. 144: 509-512 (1973), the relevant portion of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow (v) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH). An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure (P_{tp}). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance (R_t) and dynamic compliance (C_{dyn}) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and C_{dyn} was calculated using the total volume and the difference in P_{tp} at zero flow, and . R_t was calculated as the ratio of Ptp and V at midtidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., Arch. Int. Pharmacodyn. Ther. 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The B4R was then determined by calculating the concentration of histamine (mg/ml) required to reduce the C_{dyn} 50% from baseline ($PC_{50\ Histamine}$).

Example 15: Cardiovascular Effect of Anti-sense Oligo I

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.5 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent disclosure being incorporated in its entirety here by reference. A thermocouple was then inserted into the left carotid artery of each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured. A thermodilution curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20EC to determine the correctness of positioning of the thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were isolated. The femoral vein was used as a portal for drug injections, and the femoral artery for blood pressure and heart rate measurements. Once constant baseline cardiovascular parameters were established, CardiomaxJ measurements of blood pressure, heart rate, cardiac output, total peripheral resistance, and cardiac contractility were made.

Example 16: Duration of Action of Oligo I (SEQ. ID NO: 1)

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% ($PC_{50\ Adenosine}$) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized doses of (**SEQ. ID NO: 1**) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the $PC_{50\ Adenosine}$ values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

Example 17: Reduction of Adenosine A_{2b} Receptor Number by Anti-sense Oligo V

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (**SEQ ID NO:10**) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine A_{2b} receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at $p<0.05$ using Student's paired t test, and are discussed in Example 28 below.

Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)

Oligo I (**SEQ ID NO:1**) countered the effects of adenosine and eliminated sensitivity to it for adenosine amounte up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (**SEQ ID NO:1681**), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (**SEQ ID NO:1**), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at $p<0.001$, Student's paired t test. The results are discussed in Example 29 below.

RESULTS OBTAINED FOR ANTI-SENSE OLIGO I (SEQ. ID NO: 1)

Example 19: Results of Prior Work

The nucleotide sequence and other data for anti-sense oligo I (**SEQ. ID NO: 1**), which is specific for the adenosine A_1 receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (**SEQ. ID NO: 1**):

(1) The anti-sense oligo I reduces the number of adenosine A_1 receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5 below.
(2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.
(3) The Oligo I attenuates bronchial hyperresponsiveness as measured by PC_{50} histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5 above.
(4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine A_1 receptor, and has no effect at all at any dose on either the very closely related adenosine A_2 receptor or the related bradykinin B_2 receptor. This is seen in Table 5 below.
(5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (**SEQ. ID NO:1682** and **SEQ. ID NO:1683**) which have identical base composition and molecular weight but differed from the anti-sense oligo I (**SEQ ID NO: 1**) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors (A_1, A_2 or B_2).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine A_1 receptor, are unexpected results. The showings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.

Example 20: Oligo I Significantly Reduces Response to Adenosine Challenge

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A_1-selective ligand [$_3$H]DPCPX and the bradykinin B_2-selective ligand [^{3}H]NPC 17731 in membranes isolated from airway smooth muscle of A_1 adenosine receptor and B_2 bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

Table 5: Binding Characteristics of Three Anti-Sense Oligos

Treatment[1]	**A_1 receptor**		**B_2 receptor**	
	Kd	**B_{max}**	**Kd**	**Bmax**
Adenosine A_1	**Receptor**			
20 mg	0.36±0.029 nM	19±1.52 fmoles*	0.39±0.031 nM	14.8±0.99fmoles
2 mg	0.38±0.030 nM	32±2.56 fmoles*	0.41±0.028 nM	15.5±1.08
0.2 mg	0.37±0.030 nM	49±3.43 fmoles	0.34±0.024 nM	15.0±1.06
A_1MM1	**(Control)**			
20 mg	0.34±0.027 nM	52.0±3.64 fmoles	0.35±0.024 nM	14.0±1.0 fmoles
2 mg	0.37±0.033 nM	51.8±3.88 fmoles	0.38±0.028 nM	14.6±1.02
B_2A (Bradykinin	**Receptor)**			
20 mg	0.36±0.028 nM	45.0±3.15 fmoles	0.38±0.027 nM	8.7±0.62

2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
B_2MM				
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

[1] Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey=s protected t test. n = 4-6 for all groups.
* Significantly different from mismatch control- and saline-treated groups, p<0.001;
**Significantly different from mismatch control- and saline-treated groups, p<0.05.

Example 21: Dose-response Effect of Oligo I

Anti-sense oligo I (**SEQ ID NO:1**) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

Table 6: Dose-Response Effect to Anti-sense Oligo I

Total Dose (mg)	**$PC_{50\ Adenosine}$** (mg Adenosine)
Anti-sense Oligo I	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
A_1MM2 oligo (control)	
0.2	2.51±0.46
2.0	3.13± 0.71
20	3.25± 0.34

The above results were studied with the Student's paired t test and found to be statistically different, p=0.05

The oligo I (**SEQ. ID NO:1**), an anti-adenosine A_1 receptor oligo, acts specifically on the adenosine A_1 receptor, but not on the adenosine A_2 receptors. These results stem from the treatment of rabbits with anti-sense oligo I (**SEQ. ID NO.1**) or mismatch control oligo (**SEQ. ID NO:1682**; A_1MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A_1 and adenosine A_2 receptors determined as reported in Nyce & Metzger (1997), supra.

Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product

Oligo I (SEQ. ID No:1) is specific for the adenosine A_1 receptor whereas its mismatch controls had no activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (**SEQ. ID NO:1682** and **SEQ. ID NO:1683**) evidenced no effect on the $PC_{50\ Adenosine}$ value. On the contrary, the administration of anti-sense oligo I (**SEQ. ID NO:1**) showed a seven-fold increase in the $PC_{50\ Adenosine}$ value. The results clearly indicate that the anti-sense oligo I (**SEQ. ID NO: 1**) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 6 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 5). The Oligo I was also shown to be totally specific for the adenosine A_1 receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A_2 receptor or the bradykinin B_2 receptor (see, lines 8-10 of Table 6 above). In addition, the results shown in Table 6 establish that the anti-sense oligo I (**SEQ. ID NO:1**) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an

anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A_1MM2; **SEQ. ID NO:1682** and A MM3; **SEQ. ID NO:1683**) show any effect on $PC_{50\ Adenosine}$ values or on attenuating the number of adenosine A_1 receptors.

Example 23: **Effect on Aeroallergen-induced Bronchoconstriction & Inflammation**

The Oligo I (**SEQ. ID NO:1**) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID No:1) and the mismatch oligos (A_1MM2, **SEQ. ID NO:1682** and A_1MM3, **SEQ. ID NO:1682**) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits. The effect of the anti-sense oligo I (**SEQ. ID NO:1**) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%, $p<0.05$; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A_1MM2 (Control) on allergen induced airway obstruction. The effect of the anti-sense oligo I (**SEQ. ID NO:1**) on allergen-induced BHR was determined as above. As calculated from the $PC_{50\ Histamine}$ value , the anti-sense oligo I (**SEQ. ID NO:1**) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched control (61%, $p<0.05$; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A_1MM mismatch control on allergen-induced BHR was observed. The results indicated that anti-sense oligo I (**SEQ. ID NO: 1**) is effective to protect against aeroallergen-induced bronchoconstriction (house dust mite). In addition, the anti-sense oligo I (**SEQ. ID NO:1**) was also found to be a potent inhibitor of dust mite-induced bronchial hyper responsiveness, as shown by its effects upon histamine sensitivity which indicates anti- inflammatory activity for anti-sense oligo I (**SEQ. ID NO:1**).

Example 24: **Anti-sense Oligo I is Free of Deleterious Side Effects**

The Oligo I (**SEQ. ID NO:1**) was shown to be free of side effects that might be toxic to the recipient. No changes in arterial blood pressure, cardiac output, stroke volume, heart rate, total peripheral resistance or heart contractility (dPdT) were observed following administration of 2.0 or 20 mg oligo I (**SEQ. ID NO:1**). The addition, the results of the measurement of cardiac output (CO), stroke volume (SV), mean arterial pressure (MAP), heart rate (HR), total peripheral resistance (TPR), and contractility (dPdT) with a CardiomaxJ apparatus (Columbus Instruments, Ohio) were assessed. These results evidenced that oligo I (**SEQ. ID NO:1**) has no detrimental effect upon critical cardiovascular parameters. More particularly, this oligo does not cause hypotension. This finding is of particular importance because other phosphorothioate anti-sense oligonucleotides have been shown in the past to induce hypotension in some model systems. Furthermore, the adenosine A_1 receptor plays an important role in sinoatrial conduction within the heart. Attenuation of the adenosine A_1 receptor by anti-sense oligo I (**SEQ. ID NO:1**) might be expected to result, therefore, in deleterious extrapulmonary activity in response to the downregulation of the receptor. This is not the case. The anti-sense oligo I (**SEQ. ID NO:1**) does not produce any deleterious intrapulmonary effects and renders the administration of the low doses of the present anti-sense oligo free of unexpected, undesirable side effects. This demonstrates that when oligo I (**SEQ. ID NO:1**) is administered directly to the lung, it does not reach the heart in significant quantities to cause deleterious effects. This is in contrast to traditional adenosine receptor antagonists like theophylline which do escape the lung and can cause deleterious, even life-threatening effects outside the lung.

Example 25: **Long Lasting Effect of Oligo I**

The Oligo I (**SEQ. ID NO:1**) evidenced a long lasting effect as evidenced by the PC_{50} and Resistance values obtained upon its administration prior to adenosine challenge. The duration of the effect was measured for with respect to the PC_{50} of adenosine anti-sense oligo I when administered in four equal doses of 5 mg each by means of a nebulizer via an endotracheal tube, as described above. The effect of the agent is significant over days 1 to 8 after administration. When the effect of the anti-sense oligo I (**SEQ. ID

NO:1) had disappeared, the animals were administered saline aerosols (controls), and the $PC_{50\ Adenosine}$ values for all animals were measured again. Saline-treated animals showed base line PC_{50} adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (**SEQ. ID NO: 1**) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC_{50} adenosine ($p<0.05$) and resistance ($p<0.05$). These results show that anti-sense oligo I (**SEQ. ID NO:1**) has an extremely long duration of action, which is completely unexpected.

<u>Example 26</u>: Anti-sense Oligo II

Anti-sense oligo II, targeted to a different region of the adenosine A_1 receptor mRNA, was found to be highly active against the adenosine A_1-mediated effects. The experiment measured the effect of the administration of anti-sense oligo II (**SEQ. ID NO:7**) upon compliance and resistance values when 20 mg anti-sense oligo II or saline (control) were administered to two groups of allergic rabbits as described above. Compliance and resistance values were measured following an administration of adenosine or saline as described above in Example 13. The effect of the anti-sense oligo of the invention was different from the control in a statistically significant manner, $p<0.05$ using paired t-test, compliance; $p<0.01$ for resistance. The results showed that anti-sense oligo II (**SEQ. ID NO:7**), which targets the adenosine A_1 receptor, effectively maintains compliance and reduces resistance upon adenosine challenge.

<u>Example 27</u>: Antisense Oligos III and IV

Oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) were shown to be in fact specifically targeted to the adenosine A_3 receptor by their effect on reducing inflammation and the number of inflammatory cells present upon separate administration of 20 mg of the anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) to allergic rabbits as described above. The number of inflammatory cells was determined in their bronchial lavage fluid 3 hours later by counting at least 100 viable cells per lavage. The effect of anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) upon granulocytes, and upon total cells in bronchial lavage were assessed following exposure to dust mite allergen. The results showed that the anti-sense oligo IV (**SEQ. ID NO:9**) and anti-sense oligo III (**SEQ. ID NO:8**) are very potent anti-inflammatory agents in the asthmatic lung following exposure to dust mite allergen. As is known in the art, granulocytes, especially eosinophils, are the primary inflammatory cells of asthma, and the administration of anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) reduced their numbers by 40% and 66%, respectively. Furthermore, anti-sense oligos IV (**SEQ. ID NO:9**) and III (**SEQ. ID NO:8**) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A_3 agents of the invention. Inflammation is known to underlie bronchial hyperresponsiveness and allergen-induced bronchoconstriction in asthma. Both anti-sense oligonucleotides III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**), which are targeted to the adenosine A_3 receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

<u>Example 28</u>: Anti-sense Oligo V

The anti-sense oligo V (**SEQ. ID NO:10**) , targeted to the adenosine A_{2b} adenosine receptor mRNA was shown to be highly effective at countering adenosine A_{2b}-mediated effects and at reducing the number of adenosine A_{2b} receptors present to less than half.

<u>Example 29</u>: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS (SEQ. ID NO:1681)

Oligos I (**SEQ. ID NO:1**) and I-DS (**SEQ. ID NO:1681**) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (**SEQ. ID NO:1681**) was statistically significantly less effective in countering the effect of adenosine whereas oligo I (**SEQ. ID NO:1**) showed high effectiveness, evidencing a $PC_{50\ Adenosine}$ of 20 mg.

Example 30: Anti-sense Oligo VI

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A_1 receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A_1 receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A_1 receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A_1 receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The OligoVI is directed to the adenosine A_1 receptor gene, and has the following sequence: **5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO:_).** The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

Example 31: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (D. farinae) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

Example 32: Adenosine Aerosol Preparation

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:m in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC_{50} Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC_{50} values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) below.

Example 33: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the A_1 receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter, PC_{50} adenosine studies were performed on the morning of the third day and compared to pre-treatment PC_{50} values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 7 below.

Table 7: PC_{50} Adenosine before & after Aerosolized Adenosine Treatment

Treatment Time	PC_{50} Adenosine (mg)
Pre-treatment	3.0 ±2.1
Post-treatment	>20.0*

* maximum achievable dose due to adenosine insolubility in saline

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 7 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

Example 34: Conclusions

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine A_1 receptor mRNA, 1 anti-sense oligo targeting an adenosine A_{2b} receptor mRNA, and the 2 anti-sense oligos targeting an A_3 receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to. The activity of the anti-sense oligos of this invention, moreover, is specific to the target and substitutively fails to inhibit another target. In addition, the results presented also show that the administration of the present agents results in extremely low or non-existent deleterious side effects or toxicity. This represents 100% success in providing agents that are highly effective and specific in the treatment of bronchoconstriction and/or inflammation. This invention is broadly applicable in the same manner to all gene(s) and corresponding mRNAs encoding proteins involved in or associated with airway diseases. A comparison of the phosphodiester and a version of the same oligonucleotide wherein the phosphodiester bonds are substituted with phosphorothioate bonds evidenced an unexpected superiority for the phosphothiorate oligonucleotide over the phosphodiester anti-sense oligo.

Example 35: In Vivo Response to Adenosine Challenge with & without Oligo I Pretreatment

Two hyper responsive monkeys (ascaris sensitive) were challenged with inhaled adenosine, with and without pre-treatment with anti-sense oligo I (**SEQ.ID NO: 1**). The PC_{40} adenosine was calculated from the data collected as being equivalent to that amount of adenosine in mg that causes a 40% decrease in dynamic compliance in hyper-responsive airways. The Oligo I (**SEQ. ID NO:1**; EPI 2010) was subsequently administered at 10 mg/day for 2 days by inhalation. On the third day, the PC adenosine was again measured. The PC_{40} adenosine value prior to treatment with Oligo I was compared side-by-side with

to the PC_{40} adenosine taken after administration of Oligo I (Figure not shown). The results of the experiment conducted with two animals showed that any sensitivity to adenosine was completely eliminated by the administration of the oligo of this invention in one animal, and substantially reduced in the second.

Example 36: Extension of the experimental Results

The method of the present invention is also practiced with anti-sense oligonucleotides targeted to many genes, mRNAs and their corresponding proteins as described above, in essentially the same manner as given above, for the treatment of various conditions in the lungs. Examples of these are Human A2a adenosine receptor, Human A2b adenosine receptor, Human IgE receptor β, Human Fc-epsilon receptor CD23 antigen (IgE receptor), Human IgE receptor, α subunit, Human IgE receptor, Fc epsilon R, Human histidine decarboxylase, Human beta tryptase, Human tryptase-I, Human prostaglandin D synthase, Human cyclooxygenase-2, Human eosinophil cationic protein, Human eosinophil derived neurotoxin, Human eosinophil peroxidase, Human intercellular adhesion molecule-1 (CAM-1), Human vascular cell adhesion molecule 1 (VCAM-1), Human endothelial leukocyte adhesion molecule (ELAM-1), Human P Selectin, Human endothelial monocyte activating factor, Human IL3, Human IL4, Human IL5, Human IL6, Human monocyte-derived neutrophil chemotactic factor, Human neutrophil elastase (medullasin), Human neutrophil oxidase factor, Human cathepsin G, Human defensin 1, Human defensin 3, Human macrophage inflammatory protein-1-alpha, Human muscarinic acetylcholine receptor HM1, Human muscarinic acetylcholine receptor HM3, Human fibronectin, Human interleukin 8, Human GM-CSF, Human tumor necrosis factor α, Human leukotriene C4 synthase, Human major basic protein, and many more.

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

WHAT IS CLAIMED AS NOVEL & UNOBVIOUS IN UNITED STATES LETTERS PATENT IS:

1. A pharmaceutical composition, comprising

an oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies), or surfactant depletion or hyposecretion, when administered to a mammal, the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and

a pharmaceutically or veterinarily acceptable carrier or diluent.

2. The composition of claim 1, wherein the oligo is A-free.

3. The composition of claim 1, wherein the target is selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; the polypeptides being selected from the group consisting of peptide factors and transmitters, antibodies, cytokines and chemokines, enzymes, binding proteins, adhesion molecules, their receptors, and malignancy associated proteins.

4. The composition of claim 3, wherein the target is selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; wherein the polypeptides are selected from the group consisting of transcription factors, stimulating and activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding proteins, and malignancy associated proteins.

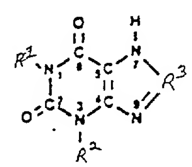
5. The agent of claim 4, wherein the encoded polypeptide(s) is(are) selected from the group consisting of adenosine receptors A1, A2a, A2b and A3, bradykinin receptors B1 and B2, Nf6B Transcription Factor, Interleukin-8 Receptor (IL-8 R), Interleukin 5 Receptor (IL-5 R), Interleukin 4 Receptor (IL-4 R), Interleukin 3 Receptor (IL-3 R), Interleukin-1β (IL-1β), Interleukin 1β Receptor (IL-1β R), Eotaxin, Tryptase, Major Basic Protein, β2-adrenergic Receptor Kinase, Endothelin Receptor A, Endothelin Receptor B, Preproendothelin, Bradykinin B2 Receptor, IgE High Affinity Receptor, Interleukin 1 (IL-1), Interleukin 1 Receptor (IL-1 R), Interleukin 9 (IL-9), Interleukin-9 Receptor (IL-9 R), Interleukin 11 (IL-11), Interleukin-11 Receptor (IL-11 R), Inducible Nitric Oxide Synthase, Cyclo-oxygenase-1 (COX 1), Cyclo-oxygenase-2 (COX-2), Intracellular Adhesion Molecule 1 (ICAM-1) Vascular Cellular Adhesion Molecule (VCAM), Rantes, Endothelial Leukocyte Adhesion Molecule (ELAM-1), Monocyte Activating Factor, Neutrophil Chemotactic Factor, Neutrophil Elastase, Defensin 1, 2 and 3, Muscarinic Acetylcholine Receptors, Platelet Activating Factor, Tumor Necrosis Factor α, 5-lipoxygenase, Phosphodiesterase IV, Substance P, Substance P Receptor, Histamine Receptor, Chymase, CCR-1 CC Chemokine Receptor, CCR-2 CC Chemokine Receptor, CCR-3 CC Chemokine Receptor, CCR-4 CC Chemokine Receptor, CCR-5 CC Chemokine Receptor, Prostanoid Receptors, GATA-3 Transcription Factor, Neutrophil Adherence Receptor, MAP Kinase, Interleukin-9 (IL-9), NFAT Transcription Factors, STAT 4, MIP-1α, MCP-2, MCP-3, MCP-4, Cyclophillins, Phospholipase A2, Basic

Fibroblast Growth Factor, Metalloproteinase, CSBP/p38 MAP Kinase, Tryptose Receptor, PDG2, Interleukin-3 (IL-3), Interleukin-1β (IL-1β), Cyclosporin A-Binding Protein, FK5-Binding Protein, α4β1 Selectin, Fibronectin, α4β7 Selectin, Mad CAM-1, LFA-1 (CD11a/CD18), PECAM-1, LFA-1 Selectin, C3bi, PSGL-1, E-Selectin, P-Selectin, CD-34, L-Selectin, p150,95, Mac-1 (CD11b/CD18), Fucosyl transferase, VLA-4, CD-18/CD11a, CD11b/CD18, ICAM2 and ICAM3, C5a, CCR3 (Eotaxin Receptor), CCR1, CCR2, CCR4, CCR5, LTB-4, AP-1 Transcription Factor, Protein kinase C, Cysteinyl Leukotriene Receptor, Tachychinnen Receptors (tach R), I6B Kinase 1 & 2, STAT 6, c-mas and NF-Interleukin-6 (NF-IL-6).

6. The composition of claim 1, wherein one or more As is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A_1, A_{2a}, A_{2b} and A_3 receptors.

7. The composition of claim 6, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH_2, SH, SO, SO_2, SO_3, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH_2, primary, secondary and tertiary amine, SH, SO, SO_2, SO_3, cycloalkyl, heterocycloalkyl and heteroaryl.

8. The composition of claim 7, wherein the pyrimidines and purines are substituted at a position selected from the group consisting of positions 1, 2, 3, 4, 7, and 8, and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R^1 and R^2 are independently H, alkyl, alkenyl or alkynyl and R^3 is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH_2-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO_2 aryl.

9. The composition of claim 8, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

10. The composition of claim 1, where one or more methylated cytocine(s) (^mC) is(are) substituted for a C in one or more CpG dinocleotide(s), if present in the oligo(s).

11. The composition of claim 1, wherein one or more mononucleotide(s) of the oligo(s) is(are) linked or modified by one or more methylphosphonate, 5'-N-carbamate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMI), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

12. The composition of claim 11, wherein the mononucleotide residues are linked by phosphorothioate residues.

13. The composition of claim 1, wherein the anti-sense oligo comprises about 7 to about 60 mononucleotides.

14. The composition of claim 1, wherein the anti-sense oligo comprises fragments 1, 3, 5, 7 and 8 to 2313 (SEQ. ID NOS: 1 through 2419).

15. The composition of claim 1, wherein the anti-sense oligo is operatively linked to, or complexed with, an agent selected from the group consisting of cell internalized or up-taken agents and cell targeting agents.

16. The composition of claim 15, wherein the cell internalized or up-taken agent is selected from the group consisting of transferrin, asialoglycoprotein and streptavidin.

17. The composition of claim 1, wherein the oligo is operatively linked to a vector that is a prokaryotic or eukaryotic vector.

18. The composition of claim 1, wherein the oligo(s) is(are) hybridized to a ribonucleic acid.

19. A cell, carrying the oligo of claim 1.

20. The composition of claim 1, wherein the carrier or diluent is selected from the group consisting of gaseous, liquid, and solid carriers or diluents.

21. The composition of claim 20, further comprising an agent selected from the group consisting of other therapeutic agents, surfactants, flavoring and coloring agents, fillers, volatile oils, buffering agents, dispersants, RNA inactivating agents, anti-oxidants, flavoring agents, propellants and preservatives.

22. The composition of claim 21, comprising one or more oligo(s), a surfactant, and a carrier or diluent for the oligo and the surfactant.

23. The composition of claim 21, wherein the the agent is an RNA inactivating agent which comprises an enzyme, optionally an ribozyme.

24. The composition of claim 1, wherein the anti-sense oligo is present in an amount of about 0.01 to about 99.99 w/w of the composition.

25. The composition of claim 1, which is a systemic or topical formulation.

26. The formulation of claim 25, selected from the group consisting of oral, intrabuccal, intrapulmonary, rectal, intrauterine, intratunor, intracranial, nasal, intramuscular, subcutaneous, intravascular, intrathecal, inhalable, transdermal, intradermal, intracavitary, implantable, iontophoretic, ocular, vaginal, intraarticular, otical, intravenous, intramuscular, intraglandular, intraorgan, intralymphatic, implantable, slow release and enteric coating formulations.

27. The formulation of claim 26, which is an oral formulation, wherein the carrier is selected from the group consisting of solid and liquid carriers.

28. The oral formulation of claim 27, which is selected from the group consisting of a powder, dragees, tablets, capsules, sprays, aerosols, solutions, suspensions and emulsions, optionally oil-in-water and water-in-oil emulsions.

29. The formulation of claim 25, which is a topical formulation, wherein the carrier is selected from the group consisting of creams, gels, ointments, sprays, aerosols, patches, solutions, suspensions and emulsions.

30. The formulation of claim 26, which is an injectable formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

31. The formulation of claim 26, which is a rectal formulation, optionally a suppository.

32. The formulation of claim 26, which is a transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

33. The transdermal formulation of claim 32, which is an iontophoretic transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions, and wherein the formulation further comprises a transdermal transport promoting agent.

34. The formulation of claim 26, which is provided in an implant, a capsule or a cartridge.

35. The composition of claim 20, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

36. The formulation of claim 20, wherein the carrier comprises a hydrophobic carrier.

37. The formulation of claim 36, wherein the carrier comprises lipid vesicles, optionally liposomes, or particles, optionally microcrystals.

38. The formulation of claim 37, wherein the carrier comprises liposomes, and the liposomes comprise the anti-sense oligo.

39. The formulation of claim 26, which is a respirable or inhalable formulation, optionally an aerosol.

40. The composition of claim 1, in single or multiple unit form.

41. The composition of claim 1, in bulk.

42. A kit, comprising

a delivery device;

in a separate container(s), the oligo(s) of claim 1; and

instructions for adding a carrier and for use of the kit.

43. The kit of claim 42, wherein the formulation is a respirable formulation and the delivery device comprises a nebulizer which delivers single metered doses of the formulation.

44. The kit of claim 43, wherein the nebulizer comprises an insufflator and the composition is provided in a piercable or openable capsule or cartridge.

45. The kit of claim 44, wherein the delivery device comprises a pressurized inhaler and the composition comprises a suspension, solution or dry formulation of the oligo.

46. The kit of claim 45, further comprising, in a separate container, an agent selected from the group consisting of other therapeutic agents, surfactants, anti-oxidants, flavoring agents, fillers, volatile oils, dispersants, antioxidants, propellants, preservatives, buffering agents, RNA inactivating agents, cell-internalized or up-taken agents and coloring agents.

47. The kit of claim 46, comprising, in separate containers, one or more oligos, one or more surfactants, and a carrier or diluent, and optionally other therapeutic agents.

48. The kit of claim 42, wherein the device is a transdermal delivery device, and the kit further comprises a transdermal delivery agent, a transdermal carrier or diluent, and instructions for preparing a transdermal delivery formulation.

49. The kit of claim 42, wherein the device is an iontophoretic delivery device, and the kit further comprises iontophoretic agents and instructions for preparing an iontophoretic formulation.

50. An in vivo method of delivering an anti-sense oligonucleotide(s) (oligo(s)) to one or more target polynucleotide(s), comprising administering into the respiratory system of a subject one or more oligo(s) that are anti-sense to the polynucleotide(s), in an amount effective to reach and hybridize to the target polynucleotide(s), and reduce the production or availability, or to increase the degradation, of the target mRNA, or to reduce the amount of the target polypeptide present in the lungs.

51. An in vivo method of delivering an anti-sense oligonucleotide (oligo) to a target polynucleotide associated with bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction, comprising administering to a subject the composition of claim 1, that comprises an amount of the oligo(s) effective to reach and hybridize to the target polynucleotide(s), and reduce or inhibit the polynucleotide(s)' transcription and/or expression and, thereby, alleviating bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction.

52. The method of claim 51, wherein the administered composition comprises an amount of the oligo(s) and is administered under conditions effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant depletion or hyposecretion, when administered to a mammal.

53. The method of claim 51, wherein the composition is administered into the subject's respiratory system.

54. The method of claim 53, wherein the composition is administered directly into the subject's lung (s).

55. The method of claim 51, wherein the administered composition comprises an amount of the oligo(s) and is administered under conditions effective to reduce the production or availability, or to increase the degradation, of the target mRNA or to reduce the amount of the target polypeptide present in the lungs.

56. The method of claim 51, wherein the agent is administered as a respirable aerosol.

57. The method of claim 51, wherein the pulmonary obstruction, and/or bronchoconstriction and\or lung inflammation, allergy(ies) and/or surfactant hypoproduction are associated with a disease or condition selected from the group consisting of pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhynitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and cancer.

58. The method of claim 57, wherein the disease or condition is associated with an allergy(ies), and the oligo is anti-sense to a target selected from the group consisting of the initiation codon,the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors or are anti-sense to the immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors mRNA; combinations of the oligo(s); and mixtures of the oligos.

59. The method of claim 57, wherein the disease or condition is associated with a malignancy or cancer, and the oligo is anti-sense to a target selected from the group consisting of the initiation codon,the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and\or encodes a malignancy associated protein, or is(are) anti-sense to the oncogene or malignancy associated protein mRNA; combinations of the oligo(s); and mixtures of the oligos and the oligo(s) is(are) administered in an amount effective to reduce either the level of the protein mRNA or of the malignancy associated protein, or to reduce the growth of or provide beneficial characteristics to malignant cells.

60. The method of claim 51, wherein the composition is administered transdermally or systemically.

61. The method of claim 60, wherein the composition is administered orally, intracavitarily, intranasally, intraanally, intravaginally, intrauterally, intraarticularly, transdermally, intrabucally, intravenously, subcutaneously, intramuscularly, intravascularly, intratumorously, intraglandularly, intraocularly, intracranial, into an organ, intravascularly, intrathecally, intralymphatically, intraotically, by implantation, by inhalation, intradermally, intrapulmonarily, intraotically, by slow release, by sustained release and by a pump.

62. The method of claim 51, wherein the subject is a non-human mammal.

63. The method of claim 51, wherein the mammal is a human.

64. The method of claim 51, wherein the oligo is administered in amount of about 0.005 to about 150 mg/kg body weight.

65. The method of claim 51, wherein the oligo is obtained by

(a) selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C;

(b) obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G nucleic acid content of up to and including about 15%; and

(c) obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an A base content of up to and including about 15%.

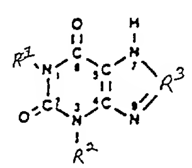
65. The method of claim 64, wherein the oligo is A-free.

66. The method of claim 51, wherein the target is selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene or a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide or oncogene mRNA; combinations of the oligo(s); and mixtures of the oligos; wherein the polypeptide isselected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules defensines, growth factors, vasoactive peptides, peptide receptors and binding proteins, and malignancy associated proteins.

67. The method of claim 51, wherein one or more As in the oligo(s) is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 0.3 of the adenosine base agonist or antagonist activity at an adenosine A_1, A_{2a}, A_{2b} and A_3 receptors.

68. The method of claim 67, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH_2, SH, SO, SO_2, SO_3, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH_2, primary, secondary and tertiary amine, SH, SO, SO_2, SO_3, cycloalkyl, heterocycloalkyl and heteroaryl.

69. The method of claim 67, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8 and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R^1 and R^2 are independently H, alkyl, alkenyl or alkynyl and R^3 is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH_2-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO_2 aryl.

70. The method of claim 69, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

71. The method of claim 51, further comprising substituting a methylated cytocine (^{m}C) for a C in one or more CpG dinucleotide(s), if present in the oligo(s).

72. The method of claim 51, further comprising substituting by, or modifying one or more nucleotide residue(s) of the oligo(s) with, methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy

(methylimino) (MOMI), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

73 The method of claim 51, further comprising operatively linking to, or complexing the oligo(s) with, an agent selected from the group consisting of cell internalized and up-taken agent(s) and cell targeting agents.

74. The method of claim 73, wherein the cell internalized or up taken agent is selected from the group consisting of transferrin, asialoglycoprotein, and streptavidin.

75. The method of claim 73, wherein the cell targeting agent is a vector, optionally a prokaryotic or eukaryotic vector.

76. A method of treating a disease or condition associated with a target selected associated with a disease or condition afflicting lung airways, comprising conducting the method of claim 56.

77. The method of claim 76, wehrein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to reduce the amount of the polypeptide present in the lungs.

78. The method of claim 77, wherein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to increase the amount of the surfactant present in the subject's lungs.

79. The composition of claim 4, wherein the oligo(s) is(are) anti-sense to the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an adenosine A1, A2a, A2b and\or A3 receptor, or anti-sense to the adenosine A1, A2a, A2b and\or A3 receptor mRNA.

80. The composition of claim 79, wherein all nucleotide linking residues are phosphorothioates.

81. The composition of claim 1, wherein the oligo is a DNA.

82. The composition of claim 1, wherein the oligo is an RNA.

83. The composition of claim 1, wherein the oligo comprises about 7 to up to about 60 mononucleotides.

84. The composition of claim 79, wherein the oligo(s) is selected from the group consisting of fragment(s) SEQ ID NOS: 1, 3, 5, 7, 8, and\or 11 through 2419, optionally wherein at least one mononucleotide residue is substituted or modified by methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino), (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMA), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate residues and/or combinations thereof.

85. The method of claim 51, wherein the oligo is administered topically to the airway, respiratory or pulmonary epithelium of the subject.

86. The composition of claim 1, wherein the oligo has a particle size of about 5-10 µm or in the range of 10-500 µm.

87. The composition of claim 1, further comprising a propellant.

88. The method of claim 50, wherein the oligo has a particle size of about 5-10 µm or in the range of 10-500 µm.

89. The method of claim 50, further comprising adding to the oligo a propellant.

90. The method of claim 51, wherein the oligo has a particle size of about 5-10 µm or in the range of 10-500 µm.

91. The method of claim 51, further comprising adding to the oligo a propellant.

LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION, ALLERGY(IES) & SURFACTANT DEPLETION

ABSTRACT OF THE INVENTION

An in vivo method of selectively delivering a nucleic acid to a target gene or mRNA, comprises the topical administration, e. g. to the respiratory system, of a subject of a therapeutic amount of an oligonucleotide (oligo) that is anti-sense to the initiation codon region, the coding region, the 5' or 3' intron-exon junctions or regions within 2 to 10 nucleotides of the junctions of the gene, or antisense to a mRNA complementary to the gene in an amount effective to reach the target polynucleotide and reducing or inhibiting expression. In addition a method of treating an adenosine mediated effect, comprises topically administering to a subject an anti-sense oligo in an amount effective to treat the respiratory, pulmonary, or airway disease. In order to minimize triggering adenosine receptors by their metabolism, the administered oligos have a low content of or are essentially free of adenosine. A pharmaceutical composition and formulations comprise the oligo anti-sense to an adenosine receptor, genes and mRNAs encoding them, genomic and mRNA flanking regions, intron and exon borders and all regulatory and functionally related segments of the genes and mRNAs encoding the polypeptides, their salts and mixtures. Various formulations contain a requisite carrier, and optionally other additives and biologically active agents. The low adenosine or adenosine free (des-A) agent for practicing the method of the invention may be prepared by selecting a target gene(s), genomic flanking region(s), RNA(s) and/or polypeptide(s) associated with a disease(s) or condition(s) afflicting lung airways, obtaining the sequence of the mRNA(s) corresponding to the target gene(s) and/or genomic flanking region(s), and/or RNAs encoding the target polypeptide(s), selecting at least one segment of the mRNA which may be up to 60% free of thymidine (T) and synthesizing one or more anti-sense oligonucleotide(s) to the mRNA segments which are free of adenosine (A) by substituting a universal base for A when present in the oligonucleotide. The agent may be prepared by selection of target nucleic acid sequences with GC running stretches, which have low T content, and by optionally replacing A in the anti-sense oligonucleotides with a "Universal or alternative base". The agent, composition and formulations are used for prophylactic, preventive and therapeutic treatment of ailments associated with impaired respiration, lung allergy(ies) and/or inflammation and depletion lung surfactant or surfactant hypoproduction, such as pulmonary vasoconstriction, inflammation, allergies, allergic rhynitis, asthma, impeded respiration, lung pain, cystic fibrosis, bronchoconstriction. The present treatment is suitable for administration in combination with other treatments, e.g. before, during and after other treatments, including radiation, chemotherapy, antibody therapy and surgery, among others. Alternatively, the present agent is effectively administered prophylactically or therapeutically by itself for conditions without known therapies or as a substitute for therapies exhibiting undesirable side effects. The treatment of this invention may be administered directly into the respiratory system of a subject so that the agent has direct access to the lungs, or by other effective routes of administration, e. g. topically, transdermally, by implantation, etc., in an amount effective to reduce or inhibit the symptoms of the ailment.